

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:08:47 ; Search time 71 Seconds  
(without alignments)  
354.076 Million cell updates/sec

Title:	US-10-712-584-2_COPY_419_483
Perfect score:	382
Sequence:	1 DAPANPCDATCKLTGTSQ.....DLDDYCNGISAGCPNPFHA 65

Scoring table:

Gapor 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	382	100.0	483	3	AAV79413	AAV79413 Southern
2	382	100.0	493	3	AAE03036	AAE03036 Agkistrod
3	346	90.6	73	2	AAW14083	AAW14083 Platelet
4	346	90.6	73	3	AAV58231	AAV58231 Korean Sm
5	346	90.6	73	5	AAE19791	AAE19791 Agkistrod
6	345	90.3	73	5	AAE19787	AAE19787 Agkistrod
7	337	88.2	73	2	AAE06494	AAE06494 Platelet
8	334	87.4	73	2	AAE06395	AAE06395 Albolabrit
9	334	87.4	73	2	AAE10106	AAE10106 Trigramin
10	334	87.4	73	2	AAE35946	AAE35946 Disintegr
11	334	87.4	73	2	AAW45500	AAW45500 Albolabrit
12	334	87.4	73	2	ADH67966	ADH67966 Compositif
13	334	87.4	73	3	AAE30598	AAE30598 Albolabrit
14	334	87.4	73	5	ABG30392	ABG30392 Glycoprot
15	334	87.4	73	7	ABU63163	ABU63163 Targeting
16	333	87.4	73	8	ADM10975	ADM10975 Ultraason
17	333	87.2	480	2	AAE42867	AAE42867 Platelet
18	326	85.3	73	2	AAE10110	AAE10110 Trigramin
19	325	85.1	96	2	AAE28703	AAE28703 Bifunctio
20	325	85.1	96	2	AAE28707	AAE28707 Bifunctio
21	325	85.1	97	2	AAE28704	AAE28704 Bifunctio
22	325	85.1	97	2	AAE28706	AAE28706 Bifunctio
23	325	85.1	99	2	AAE25153	AAE25153 Bifunctio
24	325	85.1	99	2	AAE25149	AAE25149 Bifunctio
25	325	85.1	106	2	AAE25148	AAE25148 Bifunctio

26	325	85.1	106	2	AAR25152	Aa25152	Bifunction
27	323	84.6	73	2	ADf655996	Adf655996	Snake ven
28	322	84.3	72	2	AAI10109	Aai10109	Trigramin
29	322	84.3	97	2	AA28705	Aa28705	Bifunction
30	322	84.3	97	2	AA28708	Aa28708	Bifunction
31	322	84.3	98	2	AA25154	Aa25154	Bifunction
32	322	84.3	98	2	AA25150	Aa25150	Bifunction
33	321.5	84.2	71	5	AAU75225	Aau75225	Agkistrod
34	319.5	83.6	71	2	AA25342	Aa25342	Disintegr
35	319	83.5	96	2	AA25151	Aa25151	Bifunction
36	319	83.5	96	2	AA25382	Aa25382	Bifunction
37	319	83.5	96	2	AA25147	Aa25147	Bifunction
38	318	83.2	72	1	AA291320	Aa291320	Non trig
39	307.5	80.5	73	2	AA25337	Aa25337	Disintegr
40	307	80.4	72	2	ADf65398	Adf65398	Snake ven
41	302	79.1	73	6	ABP97448	Abp97448	Disintegr
42	301.5	78.9	71	2	ADf66000	Adf66000	Snake ven
43	288	75.4	73	6	ABP97447	Abp97447	Disintegr
44	287	75.1	72	2	AAW46315	Aaw46315	Snake ven
45	287	75.1	72	2	AAW50453	Aaw50453	Snake ven

## ALIGNMENTS

## RESULT 1

ID AAY79413 standard; protein; 483 AA.

AC AAY79413

DT	26-AUG-2004	(revised)
DT	01-AUG-2000	(first entry)

DE Southern copperhead snake contortrostatin

[illegible]

OS Agkistrodon c  
OS Unidentified.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
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88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

FT /note="Pro-region; a protein comprising this region is  
FT separately claimed in Claim 3c"

FT /note= "Metalloproteinase region; a protein comprising  
 FT this region is separately claimed in Claim 3b"

FT	/note= "Encoded by CCC"
FT	419. .483
Region	

FT	this region is separately claimed in Claim 3a"
FT	457. .469
Peptide	

461-463; acts as integrin antagonist"

PN WO200018421-A1

PD 06-APR-2000.

PF 29-SEP-1999; 99WO-US022608.  
 YY

PR 29-SEP-1998; 9805-00163047.

PA (UYSCL) UNIV SOUTHERN CALIFORNIA  
XX

Markland Est. 21000

DR WPI; 2000-303389/26.  
 DR N-PSDB; AA294881.  
 XX  
 XX Novel proteins and polynucleotides representing contortrostatin useful  
 PT for inhibiting platelet aggregation, tumor metastasis and growth.  
 XX  
 XX Claim 3d; Fig 3A-C; 81pp; English.  
 XX  
 CC The present sequence is that of the Southern copperhead snake venom  
 CC disintegrin, contortrostatin, a protein that inhibits the interactions  
 CC between integrins and their receptors. The sequence was deduced from  
 CC isolated snake venom cDNA (see AA294881). The contortrostatin precursor  
 CC protein includes a pro-protein region, a metalloproteinase region which  
 CC includes a metal-binding motif, and a disintegrin region which includes  
 CC an RGD loop that acts as an integrin antagonist. Polypeptides comprising  
 CC the pro-region, the metalloproteinase region, and the contortrostatin  
 CC monomer, as well as the full-length precursor protein, can be obtained  
 CC using recombinant DNA methods. The purified proteins are used in  
 CC pharmaceutical compositions for treating diseases associated with an  
 CC integrin binding to an integrin receptor, especially to inhibit platelet  
 CC aggregation, tumour metastasis, angiogenesis, neovascularization, cell  
 CC adhesion, invasiveness, or growth (all claimed). The proteins are also  
 CC useful for treating a thrombotic disorder, e.g. preventing arterial,  
 CC venous, and microvascular thrombosis and thromboembolism, stroke,  
 CC transient ischaemic attacks, arteriosclerosis, atherosclerosis, pulmonary  
 CC embolism, aneurism, angina and myocardial infarction  
 CC  
 CC Revised record issued on 26-AUG-2004 : Correction to feature table key  
 CC  
 SQ Sequence 483 AA;  
 CC  
 CC Query Match 100.0%; Score 382; DB 3; Length 483;  
 CC Best Local Similarity 100.0%; Pred. No. 1.5e-29;  
 CC Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC 1 DAPANPCDDAATCKLTGSGCADGICCDQCKFMKEGTVCRARAGDDLDYCNGISAGCPR 60  
 CC 419 DAPANPCDDAATCKLTGSGCADGICCDQCKFMKEGTVCRARAGDDLDYCNGISAGCPR 478  
 CC  
 CC 61 NPFHA 65  
 CC 479 NPFHA 483  
 CC  
 CC Db

RESULT 2  
 AAE03036  
 ID AAE03036 standard; protein; 483 AA.  
 XX  
 AC AAE03036;  
 XX  
 XX 04-AUG-2001 (first entry)  
 DT  
 XX  
 DE Agkistrodon contortrix contortrostatin (CN) protein.  
 XX  
 KW Southern copper head snake; contortrostatin; CN; cytostatic; osteopathic;  
 KW vulnerary; disintegrin; platelet aggregation; neovascularisation; tumour;  
 KW integrin; angiogenesis; metastasis; invasiveness; growth; metastasis;  
 KW melanoma; carcinoma; sarcoma; therapy; thrombotic disease; osteoporosis;  
 KW wound healing.  
 XX  
 OS Agkistrodon contortrix.  
 XX  
 XX Key Location/Qualifiers  
 XX FH 1..190  
 XX FT Domain  
 XX FT /label= Proprotein  
 XX FT 191..410  
 XX FT Domain  
 XX FT /label= Metalloproteinase  
 XX FT 334..344  
 XX FT Binding-site  
 XX FT /label= Zinc-binding\_motif  
 XX FT 419..483  
 XX FT Domain  
 XX FT /label= Disintegrin  
 XX FT 424..433  
 XX FT Region  
 XX FT /label= Conserved\_sequence

FT /note= "This sequence is used for designing PCR primers  
 FT PCR-1 and PCR-2"  
 FT 461..463  
 FT Domain  
 FT /label= RGD\_sequence  
 XX  
 XX WO200141791-A1.  
 XX  
 XX 14-JUN-2001.  
 XX  
 XX 09-DEC-2000; 2000WO-US033367.  
 XX  
 XX 10-DEC-1999; 99US-00460295.  
 XX  
 XX 08-JUN-2000; 2000US-00591552.  
 XX  
 XX (USC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 XX Markland FS, Zhou Q;  
 XX  
 XX WPI; 2001-381494/40.  
 XX  
 XX N-PSDB; AAD07386.  
 XX  
 XX Claim 12; Fig 3; 101pp; English.  
 XX  
 CC The present sequence is contortrostatin (CN) protein from southern copper  
 CC head snake. CN, a homodimeric disintegrin binds to integrin alphavbeta5  
 CC and induces alphavbeta5-mediated tyrosine phosphorylation of CAs and FAK  
 CC in tumour cells. CN is useful for modulating the adhesion, motility, and  
 CC invasiveness of integrin expressing cells, preferably tumour cells and  
 CC for inhibiting the adhesion of integrin expressing cells to vitronectin.  
 CC The pharmaceutical composition comprising CN is useful for inhibiting  
 CC platelet aggregation, neovascularisation, angiogenesis, tumour  
 CC metastasis, invasiveness or growth, for inhibiting metastasis in  
 CC melanoma, carcinoma and sarcoma patients. It is also useful for treating  
 CC thrombotic diseases, osteoporosis, and wound healing in mammals  
 CC  
 CC Sequence 483 AA;  
 CC  
 CC Query Match 100.0%; Score 382; DB 4; Length 483;  
 CC Best Local Similarity 100.0%; Pred. No. 1.5e-29;  
 CC Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC 1 DAPANPCDDAATCKLTGSGCADGICCDQCKFMKEGTVCRARAGDDLDYCNGISAGCPR 60  
 CC 419 DAPANPCDDAATCKLTGSGCADGICCDQCKFMKEGTVCRARAGDDLDYCNGISAGCPR 478  
 CC  
 CC 61 NPFHA 65  
 CC 479 NPFHA 483  
 CC  
 CC Db

RESULT 3  
 AAM14083  
 ID AAM14083 standard; peptide; 73 AA.  
 XX  
 AC AAM14083;  
 XX  
 XX 17-OCT-2003 (revised)  
 DT  
 XX  
 DE Platelet aggregation inhibitor, Salmosin.  
 XX  
 KW Salmosin; inhibit; blood; platelet aggregation; venom; Korean;  
 KW salmosa viper; Agkistrodon halys brevicaudus; treatment; thrombosis.  
 XX  
 OS Gloydius halys brevicaudus.  
 XX  
 XX FR2736266-A1.  
 XX  
 XX 10-JAN-1997.  
 XX  
 XX

PF	24-AUG-1995;	95FR-00010049.
XX		
PR	05-JUL-1995;	95KR-00019665.
XX		
PA	(MOGA-)	MOGAM BIOTECHNOLOGY RES INST.
XX		
IN	CK, Kwang HC, Soo JL, Doo SK, Hak DK, Yung DY, Jeong HY,	
PI	Hong MM,	
XX		
DR	WP1; 1997-121376/12.	
XX		
PT	Peptide derived from Korean salmosa viper venom - useful as blood	
PT	platelet aggregation inhibitor for the management of thrombosis.	
XX		
PS	Claim 1; Page 11, 15pp; French.	
XX		
CC	This peptide, designated Salmosin, inhibits blood platelet aggregation.	
CC	It is derived from the venom of the Korean salmosa viper (Agkistrodon	
CC	halys brevicaudus). Salmosin can be used, in particular, in compositions	
CC	for management of thrombosis. Salmosin also has higher activity than	
CC	kitirin, gamma-cirgigramin and echistatin. (Updated on 17-OCT-2003 to	
CC	standardise OS field)	
XX		
Sequence	73 AA;	
XX		

[illegible]

ID	AAV58231	standard; protein; 73 AA.
XX		
AC	AAV58231;	
XX		
DT	12-SEP-2003 (revised)	
DT	27-MAR-2000 (first entry)	
XX		
DE	Korean snake venom salmosin.	
KN	Salmosin; angiogenesis; inhibitor; integrin; antagonist; disintegrin.	
XX	metastasis; cancer; tumour.	
XX		
OS	Glycydinus halys.	
XX		
FH	Key	Location/Qualifiers
FT	Region	51..53
FT		/note= "RGD motif"
XX		
PN	EP967276-A2.	
XX		
PD	29-DEC-1999.	
XX		
PF	23-JUN-1999;	99EP-00304935.
XX		
PR	23-JUN-1998;	98KR-00023778.
XX	04-JUN-1999;	99KR-00020579.
XX		
PA	(KIMD/) KIM D.	
XX		
PI	Kim D, Chung KH, Kang I;	
XX		
WP	WPI; 2000-064611/06.	
DR	N-PSDB; AAZ55609.	
DR		

XX Novel polypeptides used for antitumor therapy.  
PT  
XX  
PS Claim 1; Page 13; 24pp; English.  
XX

CC This sequence represents a 7.5 kD salmosin protein of a Korean snake,  
CC Agkistrodon halys brevicaudus. Salmosin is a disintegrin, a family of  
CC small proteins mainly derived from snake venom which contain an RGD or  
CC KGD motif (the structural motif recognised by platelet fibrinogen  
CC receptor alpha-2-b-beta-3). Disintegrins act as potent antagonists of  
CC several integrins including alpha-v-beta-3 and alpha-5-beta-1 integrins,  
CC the former being a marker of angiogenic blood vessels and certain  
CC malignant cells. Disintegrins inhibit tumour metastasis by blocking  
CC tumour cell adhesion to the extracellular matrix, and antagonism of  
CC integrin alpha-v-beta-3 can suppress tumour-induced angiogenesis.  
CC Salmosin can be used as an anticancer agent. It may be used for the  
CC inhibition or reduction of tumour cell angiogenesis, the inhibition of  
CC metastatic tumour formation and the inhibition or reduction of metastatic  
CC tumour growth. Nucleotides encoding salmosin may be used in gene therapy  
CC applications. Many types of cancer may be treated with salmosin or  
CC nucleotides encoding it, including leukemia and cancers of the breast,  
CC ovary, uterus, skin, lung, larynx, colon, pancreas, testis, liver, brain,  
CC muscle and bone. (Updated on 12-SEP-2003 to standardise OS field)

Query Match	90.6%	Score 346	DB 3	Length 73
Best Local Similarity	87.5%	Pred. No. 9.4e-27		
Matches	56	Conservative	5	Mismatches 3, Indels 0, Gaps 0.
Qy	2	APANPCCDDATCKLTGTSGCCADGLCCDQCCKFMKEGTVCRPRAGDDLDYNCGISAGCPRN	61	
	:			
Db	10	SPGNPCDDATCKLRGAGCAEGLCCQCKCFMKEGTCRRPRAGDDLDYNCGISAGCPRN	69	
	:			
Qy	62	PFHA	65	
	:			
Db	70	PFHA	73	

RESULT	5
AAE19791	
ID	AAE19791 standard; protein; 73 AA.
XX	
AC	AAE19791;
XX	
DT	29-AUG-2003 (revised)
DT	18-JUN-2002 (first entry)
DE	Agkistrodon halys brevicaudus salmosin protein.
XX	
KM	Korean snake; saxatillin; anticoagulant; cytostatic; venom; anti-tumour
KM	platelet aggregation; angiogenesis; salmosin; cytotoxicity.
OS	Gloydius halys brevicaudus.
PN	W0200214488-A1.
PD	
21-FEB-2002.	
Pf	26-JUL-2000; 2000WO-KR000809.
PR	26-JUL-2000; 2000WO-KR000809.
PA	(CHUN/) CHUNG K.
(KIMD.)	KIM D.
PI	Hong S, Koh Y, Sohn Y, You W, Jang Y, Huh C;
DRI	WPI; 2002-241903/29.
PT	New cDNA encoding Saxatillin protein derived from venom of Korean snake
PT	Agkistrodon saxatilis emeljanov, useful as anti-platelet aggregation
agent and anti-tumor agent.	

```
XX Example 5; Page 38-39; 41pp; English.
PS
XX
CC The invention relates to a cDNA encoding Saxatillin protein derived from
CC venom of Korean snake Agkistrodon saxatilis emelianov. The cDNA is useful
CC for as an anti-tumour agent and for effectively suppressing platelet
CC aggregation which makes it possible as and an active ingredient of anti-
CC platelet agent. Saxatillin is useful for inhibiting angiogenesis induced
CC by tumour and for inhibiting tumour without cytotoxicity. The present
CC sequence is Agkistrodon halys brevicaudus salmosin protein. (Updated on
CC 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 73 AA;
Query Match          90.6%; Score 346; DB 5; Length 73;
Best Local Similarity 87.5%; Pred. No. 9.4e-27;
Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 APANPCDAATCKLTTGSCADGCLCCDQCKFMKEGTVCRARAGDDLDDYCNGISAGCPRN 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 10 SPGNPCDAATCKLRGAQCAEGLCCDQCFMKEGTICRRARAGDDLDDYCNGISAGCPRN 69
QY 62 PFHA 65
   ||||
Db 70 PFHA 73

RESULT 6
AAE19787
ID AAE19787 standard; protein; 73 AA.
XX
XX AAE19787;
XX
DT 29-AUG-2003 (revised)
DT 07-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)
XX
XX Agkistrodon saxatilis emelianov saxatillin protein.
XX
XX Korean snake; saxatillin; anticoagulant; cytostatic; venom; anti-tumour;
XX platelet aggregation; angiogenesis; cytotoxicity.
XX
XX Gloydius halys.
XX
XX Key Location/Qualifiers
XX FH Misc-difference 1..3
XX FT note="Encoded by GGA"
XX
XX WO200214488-A1.
XX
XX 21-FEB-2002.
XX
XX 26-JUL-2000; 2000WO-KR000809.
XX
XX 26-JUL-2000; 2000WO-KR000809.
XX
XX (CHUN/) CHUNG K.
XX PA (KIMD/) KIM D.
XX
XX Hong S, Koh Y, Sohn Y, You W, Jang Y, Huh C;
XX
XX WPI; 2002-241903/29.
XX
XX N-PSDB; AAD31060.
XX
XX New cDNA encoding Saxatillin protein derived from venom of Korean snake
XX Agkistrodon saxatilis emelianov, useful as anti-platelet aggregation
XX agent and anti-tumour agent.
XX
XX Claim 2; Page 35; 41pp; English.
XX
XX The invention relates to a cDNA encoding Saxatillin protein derived from
XX venom of Korean snake Agkistrodon saxatilis emelianov. The cDNA is useful
XX for as an anti-tumour agent and for effectively suppressing platelet
```

```
CC aggregation which makes it possible as and an active ingredient of anti-
CC platelet agent. Saxatillin is useful for inhibiting angiogenesis induced
CC by tumour and for inhibiting tumour without cytotoxicity. The present
CC sequence is Agkistrodon saxatilis emelianov saxatillin protein. (Updated
CC on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 73 AA;
Query Match          90.3%; Score 345; DB 5; Length 73;
Best Local Similarity 87.5%; Pred. No. 1.2e-26;
Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 APANPCDAATCKLTTGSCADGCLCCDQCKFMKEGTVCRARAGDDLDDYCNGISAGCPRN 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 10 APANPCDAATCKLRGAQCAEGLCCDQCFMKEGTICRMARAGDDMDYCNGISAGCPRN 69
QY 62 PFHA 65
   ||||
Db 70 PFHA 73

RESULT 7
AAR06494
ID AAR06494 standard; protein; 73 AA.
XX
XX AAR06494;
XX
AC 25-MAR-2003 (revised)
DT 04-JAN-1991 (first entry)
XX
XX Platelet aggregation inhibitor.
XX
XX Snake venom; thromboxan A2; thrombosis; anti-coagulant.
XX
XX Synthetic.
XX
XX WO9008772-A.
XX
XX 09-AUG-1990.
XX
XX 27-JAN-1989; 89US-00303585.
XX
XX 27-JAN-1989; 89US-00303585.
XX
XX 27-JAN-1989; 89US-00303585.
XX
XX 27-JAN-1989; 89US-00303590.
XX
XX 01-NOV-1989; 89US-00430313.
XX
XX (UYBO-) UNIV BOSTON.
XX PA (BIOC) BIOGEN INC.
XX
XX Maraganore J, Jakubowski J, Chao B;
XX
XX WPI; 1990-260891/34.
XX
XX N-PSDB; AAO05730.
XX
XX Pure platelet activation inhibiting polypeptide from snake venom - used
XX for preventing agglutination and release in vivo or vitro, and new
XX recombinant dna encoding it.
XX
XX Claim 3; Fig 9; 73pp; English.
XX
XX The sequence is deduced from the coding strand of a synthetic gene for a
XX polypeptide inhibitor of platelet activation. The polypeptide is
XX analogous to that obtd. from the venom of Agkistrodon P. piscivorus
XX (North American Water Moccasin). The gene can be used to produce
XX recombinant inhibitor or fusion proteins with eg. hirudin derive. These
XX can be used to decrease/ inhibit platelet aggregation and release in vivo
XX or in vitro. Usual dose is 0.01-100 mg/kg body wt. The recombinant
XX protein can also be used to coat the surfaces of invasive medical
XX devices. It can also block stenosis and spasm at the site of thrombosis (
XX by inhibiting the release of thromboxan A2 ). See also AAR06508. (Updated
XX on 25-MAR-2003 to correct PA field.)
```

SQ Sequence 73 AA;

Query Match 88.2%; Score 337; DB 2; Length 73;  
 Best Local Similarity 87.3%; Pred. No. 7.2e-26;  
 Matches 55; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRARGLDDYCNGISACCPN 61  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 11 SPENPCDDAATCKLRGACGAGLCCDCKFMKEGTVCRARGLDDYCNGISACCPN 70  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 62 PFH 64  
 :|||  
 DB 71 PFH 73  
 :|||

RESULT 8

AAR06395

ID AAR06395 standard; protein; 73 AA.

AC AAR06395;

XX 25-MAR-2003 (revised)

DT 13-DEC-1990 (first entry)

XX Albolabrin.

DE Fibrinogen binding; inhibitor; platelet aggregation; thrombosis;

KM Viper venom.

XX Trimeresurus albolabris.

XX EP382451-A.

XX 16-AUG-1990.

XX 05-FEB-1990; 90EP-00301181.

XX 07-FEB-1989; 89US-00307642.

XX (MERI ) MERCK &amp; CO INC.

PA (UTEM ) UNIV TEMPLE.

PA (FRIE/) FRIEDMAN P A.

XX Friedman PA, Jacobs JW, Gould RJ, Polokoff MA, Gan ZR;

PI Niewiarowski S, Holt JC, Rucinaki B;

XX WPI; 1990-248351/33.

DR Viper venom polypeptide(s) - useful for inhibiting fibrinogen binding to

XX human platelets and inhibiting fibrinogen-induced aggregation.

XX Claim 2; Page 13; 13pp; English.

XX The peptide is prepd. from the venom of the viper T. albolabris or may be  
 CC prepd. by genetic engineering or solid phase synthesis. It inhibits both  
 CC fibrin binding to human platelets and fibrinogen-induced aggregation of  
 CC human platelets. It is eliminated from the circulation rapidly and is  
 CC therefore useful in situations where a strong antithrombotic action of  
 CC short duration is needed, e.g. in surgery on peripheral arteries, in  
 CC cardiovascular surgery and the interaction of platelets with artificial  
 CC surfaces. See also AAR06389-97. (Updated on 25-MAR-2003 to correct PA  
 CC field.)

XX Sequence 73 AA;

SQ Query Match

Best Local Similarity 87.4%; Score 334; DB 2; Length 73;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRARGLDDYCNGISACCPN 61  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 10 SPANPCDDAATCKLRGACGAGLCCDCKFMKEGTVCRARGLDDYCNGISACCPN 69  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 PFHA 65  
 :|||  
 DB 70 PLHA 73  
 :|||

RESULT 9

AAR10106

ID AAR10106 standard; protein; 73 AA.

XX AAR10106;

XX 13-MAR-1991 (first entry)

XX Trigramin-gamma.

DE Platelet aggregation inhibitor; snake venom; fibrin binding; inhibition;

KM GP IIA; GP IIA; hypercoagulation.

XX Synthetic.

XX WO9015072-A.

XX 13-DEC-1990.

XX 07-JUN-1989; 89US-00362718.

XX 07-JUN-1989; 89US-00362718.

XX (GETH ) GENENTECH INC.

XX Lazarus R, Dennis M;

XX WPI; 1991-007159/01.

XX N-PSDB; AAQ10160.

XX Platelet aggregation inhibiting amino acid sequences - are derived from

XX snake venom and inhibit fibrinogen binding to GP IIA-GP IIA.

XX Disclosure; Fig 1; 91pp; English.

XX The sequence was produced by recombinant techniques using a synthetic  
 CC gene prepd. from 10 oligonucleotides based on the amino acid sequence  
 CC determined by Edman degradation. The recombinant trigramin-gamma is used  
 CC in treatment of hypercoagulation-related states. See also AAR10107-R10113

XX Sequence 73 AA;

Query Match 87.4%; Score 334; DB 2; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 1.4e-25;

Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRARGLDDYCNGISACCPN 61  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 10 SPANPCDDAATCKLRGACGAGLCCDCKFMKEGTVCRARGLDDYCNGISACCPN 69  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 62 PFHA 65  
 :|||  
 DB 70 PLHA 73  
 :|||

RESULT 10

AAR53946

ID AAR53946 standard; peptide; 73 AA.

XX AAR53946;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

XX 21-DEC-1994 (first entry)

XX Disintegrin peptide #14.

XX Disintegrin; Viperidae; snake; integrin; inhibitor; fibrinogen;

KW integrin binding sites; GP IIb/IIIa; human; platelets; radiolabel;  
 KW treatment; diagnosis; venous; arterial; thrombi; pulmonary emboli;  
 KW tumours; abscesses; thrombus component.  
 XX  
 OS Trimeresurus albolabris.  
 XX  
 PN WO9409036-A1.  
 XX  
 PD 28-APR-1994.  
 XX  
 PF 05-OCT-1993; 93WO-US009523.  
 XX  
 PR 19-OCT-1992; 92US-00965674.  
 XX  
 PA (UTEM ) UNIV TEMPLE.  
 XX  
 PI Knight LC, Maurer AH;  
 XX  
 DR WPI; 1994-151248/18.  
 XX  
 PT Radio-labelled polypeptide(s) derived from Viperidae disintegrin(s) - for  
 PT treatment and diagnosis of venous and arterial thrombi, pulmonary emboli  
 PT and tumours or abscesses having a thrombus component.  
 XX  
 PS Claim 28; Page 48; 62pp; English.  
 XX  
 CC The sequences given in AAR53933-46 are disintegrin peptides. Disintegrins  
 CC are low molecular weight proteins from the Viperidae family of snakes  
 CC which bind integrin proteins similar to the endogenous messenger and  
 CC structurally interactive molecules. Disintegrins are competitive  
 CC inhibitors of biomolecules, such as fibrinogen, for integrin binding  
 CC sites such as GP IIb/IIIa on human platelets. Disintegrins contain the  
 CC tripeptide sequence Arg-Gly-Asp. Radiolabelled disintegrin peptides can  
 CC be used for the treatment and diagnosis of venous and arterial thrombi.  
 CC pulmonary emboli and tumours or abscesses that have a thrombus component.  
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to  
 CC correct OS field.)  
 XX  
 SQ Sequence 73 AA;  
 XX  
 Query Match 87.4%; Score 334; DB 2; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 1.4e-25;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 OY 2 APANPCDAATCKLTGSGCADGLCCDQCKFMKEGTGCRARAGDDLDYCNGISAGCPRN 61  
 DB 10 SPANCCDAATCKLPGAGCGRGLCCDQCSFMKKGTRICRRAGDDLDYCNGISAGCPRN 69  
 OY 62 PFHA 65  
 DB 70 PLHA 73  
 XX  
 RESULT 11  
 AAW45500  
 ID AAW45500 standard; peptide; 73 AA.  
 XX  
 AC AAW45500;  
 XX  
 DT 20-MAY-1998 (first entry)  
 XX  
 DE Albolabrin peptide targeting ligand.  
 XX  
 KW Contrast agent; targeted composition; diagnosis; diseased tissue;  
 KW glycoprotein GPIIb/IIIa receptor; albolabrin.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9640285-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96WO-US009938.

XX  
 PR 07-JUN-1995; 95US-00497684.  
 PR 01-MAY-1996; 96US-00640464.  
 XX  
 PA (IMAR-) IMARX PHARM CORP.  
 XX  
 PI Unger EC, Shen D, Wu G;  
 XX  
 DR WPI; 1997-077233/07.  
 XX  
 PT Contrast agent or targeted compsn. for imaging or treating diseased  
 PT tissue - comprising lipid, protein or polymer, a gas, and a targeting  
 PT ligand e.g. a protein, peptide, saccharide or steroid.  
 XX  
 PS Disclosure; Page 57; 175pp; English.  
 XX  
 CC This sequence represents a targeting ligand. The invention relates to a  
 CC contrast agent for diagnostic imaging or a target composition which  
 CC comprises: (i) a lipid, protein or polymer and (ii) a gas, in combination  
 CC with (iii) a targeting ligand (TL). TL targets cells or receptors  
 CC selected from myocardial, endothelial, epithelial and tumour cells and  
 CC the glycoprotein GPIIb/IIIa receptor. Also claimed are: a composition  
 CC comprising vesicles containing (i) - (iii) and an aqueous carrier; a  
 CC targeted vesicle composition comprising a fluorinated gas and a targeting  
 CC ligand (TL) which targets tissues or receptors; a formulation for  
 CC therapeutic or diagnostic use comprising (i)-(iii) and a bioactive agent;  
 CC and a method for providing an image of an internal region of a patient,  
 CC or for diagnosing the presence of diseased tissue, comprising: (a)  
 CC administration of a composition as above; and (b) scanning the patient  
 CC using ultrasound to obtain a visible image of the region or diseased  
 CC tissue. The methods and compounds are useful for imaging or diagnosing  
 CC the presence of diseased tissue, especially myocardial, endothelial or  
 CC epithelial tissue but also gastrointestinal and cardiovascular regions.  
 CC In particular the ligand targets regions of arteriosclerosis. Stabilised  
 CC vesicles are particularly useful for perfusion imaging. The vesicles may  
 CC also be used to deliver active agents to an intended target such as  
 CC tissue or a receptor, and ultrasound can then be used to promote rupture  
 CC of the vesicles and release a bioactive or diagnostic agent  
 XX  
 SQ Sequence 73 AA;  
 XX  
 Query Match 87.4%; Score 334; DB 2; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 1.4e-25;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 OY 2 APANPCDAATCKLTGSGCADGLCCDQCKFMKEGTGCRARAGDDLDYCNGISAGCPRN 61  
 DB 10 SPANCCDAATCKLPGAGCGRGLCCDQCSFMKKGTRICRRAGDDLDYCNGISAGCPRN 69  
 OY 62 PFHA 65  
 DB 70 PLHA 73  
 XX  
 RESULT 12  
 ADH67966  
 ID ADH67966 standard; peptide; 73 AA.  
 XX  
 AC ADH67966;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE Composition targeting ligand peptide Albolabrin.  
 XX  
 KW bioactive agent; anionic lipid; cationic counter ion;  
 KW lipid covalently bonded to a polymer; ultrasound; charged lipid;  
 KW targeted drug delivery; diagnostic imaging; targeting ligand;  
 KW GPIIb/IIIa receptor; diagnosis; vascular thrombosis; clot.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9842383-A1.  
 XX

[illegible]

PD	10-AUG-2000.
XX	
XX	02-FEB-2000; 2000WO-US002620.
PF	
XX	
XX	03-FEB-1999; 99US-00243640.
PR	
XX	
XX	(IMAR-) IMARX PHARM CORP.
PA	
XX	
XX	Unger EC, Wu Y;
PI	
DR	WPI; 2000-532867/48.
XX	
PT	ultrasound method, useful for diagnosis of e.g. thrombi or carcinomas,
XX	
XX	uses different types of energy for priming and interrogating the subject.
PS	
XX	Disclosure; Page 70; 211pp; English.
XX	
CC	The present invention describes an ultrasound method comprising: (i)
CC	administering a targeted vesicle composition (A); and (ii) scanning the
CC	subject by exposure to a first type of ultrasound energy and then
CC	interrogating with a second type of ultrasound energy. (A) consists of a
CC	vesicle comprising a lipid, protein or polymer, encapsulating a gas, in
CC	combination with a targeting ligand. The method is used to detect: (i) a
CC	thrombus (particularly old or echogenic); (ii) a low concentration of
CC	vesicles; or (iii) vesicles targeted to endothelial tissue, particularly
CC	those containing integrins associated with malignancy or inflammation in
CC	early or small lesions, e.g. atherosclerotic plaque or ovarian,
CC	endometrial or other carcinomas. The method increases the signal from
CC	microbubbles and reduces background noise. The present sequence
CC	represents a targeting ligand peptide which is used in the method of the
CC	present invention
XX	
XX	Sequence 73 AA;
SQ	
Query Match	87.4%; Score 334; DB 3; Length 73;
Best Local Similarity	84.4%; Pred. No. 1,4e-25;
Matches	54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
OY	2 APANPCDDAATCKLTGSGCADGLCDQCKFMKEGTVCRPARGDDLDYCNGISAGCPRN 61
DB	10 SPANPCDDAATCKLTGSGCADGLCDQCKFMKEGTVCRPARGDDLDYCNGISAGCPRN 69
OY	62 PFHA 65
DB	70 PLHA 73
RESULT 14	
ABG30392	
ID	ABG30392 standard; protein; 73 AA.
XX	
XX	ABG30392;
XX	
XX	07-OCT-2002 (first entry)
XX	
DE	Glycoprotein GpIbIIIA targeting ligand Albolabrin.
XX	
XX	Target vesicle; diagnostic imaging; thrombus; cancer; albolabrin;
KW	arteriosclerosis; atherosclerotic plaque; infarcted myocardium;
KW	glycoprotein GpIbIIIA receptor; targeting ligand.
XX	
OS	Unidentified.
XX	
FN	WO200236161-A2.
XX	
XX	10-MAY-2002.
PD	
XX	
PF	17-OCT-2001; 2001WO-US032308.
XX	
XX	30-OCT-2000; 2000US-0069679.
XX	
XX	(IMAR-) IMARX THERAPEUTICS INC.
XX	

PI Unger EC, Matsunaga TO, Schumann PA;  
XX  
XX MPI: 2002-489986/52.  
XX  
XX  
PT New targeted compound useful in target vesicle composition for imaging a  
PT thrombus in a region of a patient has a combination of hydrophobic  
PT compound, hydrophilic polymer and targeting ligand.  
XX  
XX  
PS Disclosure: Page 68; 206pp; English.  
XX  
XX This invention relates to a novel targeted compound having a combination  
CC of hydrophobic compound, hydrophilic polymer and targeting ligand. The  
CC invention also comprises a target vesicle composition comprising a lipid,  
CC protein or polymer gas filled vesicles in an aqueous carrier, a method  
CC for imaging a thrombus in a region of a patient involving administering  
CC to the patient a target vesicle composition and scanning the region  
CC (preferably cardiac region) with diagnostic imaging (preferably  
CC diagnostic ultrasound) and a method for lysing a thrombus in a blood  
CC vessel. The invention also comprises a method for providing an image of  
CC an internal region of a patient which can be used to obtain a visible  
CC image of a region (preferably arteriosclerosis, atherosclerotic plaque,  
CC infarcted myocardium or a cancer cell) and a method for diagnosing the  
CC presence of disease tissue in a patient involving administering a target  
CC vesicle composition and scanning the patient using ultrasound to obtain a  
CC visible image of the region. The methods of the invention may be used for  
CC imaging a thrombus in a region of a patient, lysing a thrombus in a blood  
CC vessel, diagnosing the presence of diseased tissue in a patient and for  
CC the therapeutic delivery in vivo of a bioactive agent. The compounds of  
CC the invention are easily synthesised and have diagnostic efficacy,  
CC enhanced biocompatibility and/or improved targeting efficacy over prior  
CC art methods. The present sequence represents a glycoprotein gp130  
CC receptor targeting ligand albolabrin used in the method of the invention  
XX  
SQ Sequence 73 AA:  
Query Match 87.4%; Score 334; DB 5; Length 73;  
Best Local Similarity 84.4%; Pred. No. 1.4e-25;  
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 2 APANPCDAAATCKLTGSGCAGDLCCDQCKFMKEGTVCRARAGDDLDYCNGISAGCPRN 61  
DB 10 SPANPCDAAATCKLPGACGCGSLCCDQCSFMKGTICRRARAGDDLDYCNGISAGCPRN 69  
QY 62 PFHA 65  
| | |  
DB 70 PLHA 73  
XX  
RESULT 15  
ABU63163  
ID ABU63163 standard; protein; 73 AA.  
XX  
AC ABU63163;  
XX  
DT 17-SEP-2003 (first entry)  
XX  
DE Targeting ligand #13 used in novel diagnostic ultrasound method.  
XX  
KM Ultrasound method; targeted vesicle composition; targeting ligand;  
KM ultrasound scanning; dual frequency ultrasound insonation; micelle;  
KM liposome; phospholipid; ultrasound energy; vesicle oscillation;  
KM reflected ultrasound signal; ultrasound diagnosis; echogenic thrombus;  
KM endothelial tissue; epithelial cell; tumour cell; myocardial cell;  
KM integrin; malignancy; inflammation; heart; diseased tissue; imaging;  
KM gastrointestinal region; lymphatic system.  
XX  
OS Synthetic.  
XX  
PN US6521211-B1.  
XX  
PD 18-FEB-2003.  
XX  
PF 03-FEB-1999; 99US-00243640.

XX  
XX 07-JUN-1995; 95US-00497684.  
PR 01-MAY-1996; 96US-00640464.  
PR 06-JUN-1996; 96US-00660032.  
PR 06-FEB-1998; 98US-0079913P.  
PR 22-DEC-1998; 98US-00218660.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB MEDICAL IMAGING INC.  
XX  
PI Unger EC, Wu Y;  
XX  
XX MPI: 2003-531036/50.  
XX  
PT Ultrasound diagnosis, by administering targeted vesicle composition with  
PT vesicles encapsulating gas, in combination with targeting ligand, to a  
PT patient, and scanning patient by dual frequency ultrasound insonation.  
XX  
PS Disclosure: Col 50; 96pp; English.  
XX  
XX The present invention relates to a novel ultrasound method which involves  
XX administering to a patient a targeted vesicle composition which comprises  
XX vesicles encapsulating a gas, in combination with a targeting ligand, and  
XX scanning the patient using dual frequency ultrasound insonation. The  
XX vesicles themselves comprise a lipid, protein or polymer, and are  
XX selected from liposomes and micelles. The vesicles may comprise a  
XX phospholipid selected from dioleoylphosphatidylcholine,  
XX dimyristoylphosphatidylcholine, dipalmitoylphosphatidylcholine,  
XX distearoylphosphatidylcholine, dipalmitoylphosphatidylethanolamine,  
XX dioleoylphosphatidylethanolamine, N-  
XX succinyldioleoylphosphatidylethanolamine, 1-hexadecyl-2-  
XX palmitoylglycerophosphoethanolamine and phosphatidic acids. The method of  
XX scanning involves exposing the patient to a first ultrasound energy  
XX having a first insonation frequency to cause the vesicle to oscillate,  
XX and then subsequently, while the vesicle is oscillating, exposing the  
XX patient to a second ultrasound energy having a second insonation  
XX frequency that is different from the first insonation frequency, and  
XX detecting the reflected ultrasound signal. The method is useful for  
XX ultrasound diagnosis, for detection of a thrombus or enhancement of  
XX thrombus (e.g. old or echogenic thrombus) and for detecting vesicles  
XX targeted to epithelial cells, tumour cells, myocardial cells, and  
XX endothelial tissue including integrins associated with malignancy or  
XX inflammation. The method is also useful for diagnosing the presence or  
XX absence of diseased tissue in a patient, and for imaging one or more  
XX regions of a patient, such as for providing images of the heart,  
XX gastrointestinal region or lymphatic systems. ABU63151-ABU63172 represent  
XX targeting ligands that may be used in the method of the present invention  
XX  
SQ Sequence 73 AA:  
Query Match 87.4%; Score 334; DB 7; Length 73;  
Best Local Similarity 84.4%; Pred. No. 1.4e-25;  
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 2 APANPCDAAATCKLTGSGCAGDLCCDQCKFMKEGTVCRARAGDDLDYCNGISAGCPRN 61  
DB 10 SPANPCDAAATCKLPGACGCGSLCCDQCSFMKGTICRRARAGDDLDYCNGISAGCPRN 69  
QY 62 PFHA 65  
| | |  
DB 70 PLHA 73  
XX  
Search completed: November 3, 2005, 08:15:50  
Job time : 75 secs





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Query Match 51: 98.0%; Score 336; DB 2; Length 484;
Best Local Similarity 90.2%; Pred. No.1.2e-25;
Matches 55; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 5 NPCCDAATCKLTTSQCADGLCCDQCKEMKEGTVCRRARGDLDLYCNGISAGCPNPFH 64
DB 424 NPCCDAATCKLTTSQCADGLCCDQCKEMKEGTVCRRARGDLDLYCNGISAGCPNPFH 483

OY 65 A 65
DB 484 A 484

RESULT 3
A23731
aloblabrin - green pit viper
C:Species: Trimeresurus alboblabris (green pit viper)
C:Date: 28-Feb-1992 #sequence_revision 23-Aug-1997 #text_change 09-Jul-2004
C:Accession: A23731; S43021
R:Calvente, J.J.; Schaeffer, W.; Soszka, T.; Lu, W.; Cook, J.J.; Jameson, B.A.; Niewiarowski
Biochemistry 30, 5225-5229, 1991
A:Title: Identification of the disulfide bond pattern in alboblabrin, an RGD-containing
A:Reference number: A23731; PMID:91242430; PMID:2036389
A:Accession: A23731
A:Molecule type: protein
A:Residues: 1-73 <CAL>
A:Cross-references: UNIPROT:P17496
R:Jalaja, M.; Smith, K.J.; Lu, X.; Williams, J.A.; Trayer, H.; Trayer, I.P.; Hyde, E.I.;
Eur. J. Biochem. 218, 853-860, 1993
A:Title: (1)H-NMR studies and secondary structure of the RGD-containing snake toxin, alboblabrin
A:Reference number: S43021; PMID:94109384; PMID:8281937
A:Accession: S43021
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-73 <JAS>
C:Function:
A:Description: inhibits cell adhesion and platelet aggregation
C:Superfamily: unassigned disintegrins; disintegrin homology
C:Keywords: venom
F:1-69/Domain: disintegrin homology (Fragment) <DIS>
F:51-53/Region: cell attachment (R-G-D) motif
F:29-59,47-66/Disulfide bonds: #status experimental

Query Match 87.4%; Score 334; DB 2; Length 73;
Best Local Similarity 84.4%; Pred. No.4.8e-26;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 2 APANCCAAATCKLTTSQCADGLCCDQCKEMKEGTVCRRARGDLDLYCNGISAGCPN 61
DB 10 APANCCAAATCKLTTSQCADGLCCDQCKEMKEGTVCRRARGDLDLYCNGISAGCPN 69

OY 62 PFHA 65
DB 70 PLHA 73

RESULT 4
E35982
trigramin gamma - Indian green tree viper
C:Species: Trimeresurus gramineus (Indian green tree viper)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Aug-2004
C:Accession: E35982
R:Dennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.; Napier, M.A.; Deisher, T.A.; B
Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990
A:Title: Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms: evidence
A:Reference number: A35982; PMID:90207217; PMID:2320569
A:Accession: E35982
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-73 <DEN>
A:Cross-references: UNIPROT:P17496
C:Superfamily: disintegrin homology

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F:1-69/pomatin disintegrin homology (fragment) <DIS>
F:51-53/Region: cell attachment (R-G-D) motif

Query Match      87.4%; Score 334; DB 2; Length 73;
Best Local Similarity 84.4%; Pred. No. 4.0e-26;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY      2  APANPCDDAATCKLTTSQCADGLCCDQCKFMKEGTVCRARAGDDLDYDNGISAGCPRN 61
      10 SPANPCDDAATCKLTPAGCCBGLCCDQCKFMKGTTCRRARAGDDLDYDNGISAGCPRN 69
      62 PFHA 65
      70 PLHA 73

RESULT 5
A:Accession: A59411
A:Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Glycydus halys brevicandus
C:Species: Glycydus halys brevicandus
C:Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 09-Jul-2004
C:Accession: A59411
R:Terada, S.
Fukuka Univ. Sci. Reports 30, 71-78, 2000
A:Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Glycydus halys brevicandus
A:Reference number: A59409
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-71 <TER>
A:Cross-references: UNIPROT:Q90220
C:Keywords: anticoagulant; integrin inhibitor; venom

Query Match      87.2%; Score 333; DB 2; Length 71;
Best Local Similarity 84.4%; Pred. No. 5.9e-26;
Matches 54; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY      2  APANPCDDAATCKLTTSQCADGLCCDQCKFMKEGTVCRARAGDDLDYDNGISAGCPRN 61
      8  SPANPCDDAATCKLRGACBGLCCDQCKFMKGTVCRTARAGDDMDYDNGISAGCPRN 67
      62 PFHA 65
      68 PFHA 71

RESULT 6
A:Accession: A59410
A:Title: Platelet aggregation disintegrin (brevicaudin) 1b, venom - Glycydus halys brevicandus
C:Species: Glycydus halys brevicandus
C:Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 09-Jul-2004
C:Accession: A59410
R:Terada, S.
Fukuka Univ. Sci. Reports 30, 71-78, 2000
A:Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Glycydus halys brevicandus
A:Reference number: A59409
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-73 <TER>
A:Cross-references: UNIPROT:Q90220
C:Keywords: anticoagulant; integrin inhibitor; venom

Query Match      87.2%; Score 333; DB 2; Length 73;
Best Local Similarity 84.4%; Pred. No. 6e-26;
Matches 54; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY      2  APANPCDDAATCKLTTSQCADGLCCDQCKFMKEGTVCRARAGDDLDYDNGISAGCPRN 61
      10 SPANPCDDAATCKLRGACBGLCCDQCKFMKGTVCRTARAGDDMDYDNGISAGCPRN 69
      62 PFHA 65
      70 PLHA 73

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Db 70 PFHA 73

## RESULT 7

D35982 trigramin beta-2 - Indian green tree viper

N:Contains: trigramin beta-1

C:Species: Trimeresurus gramineus (Indian green tree viper)

C&gt;Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 16-Aug-2004

C:Accession: D35982; C35982

R:Demis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.; Napier, M.A.; Deisher, T.A.; Bu

Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990

A&gt;Title: Platelet glycoprotein IIb/IIIa protein antagonists from snake venoms: evidence

A:Reference number: A35982; MUID:90207217; PMID:2320569

A:Accession: D35982

A:Molecule type: protein

A:Residues: 1-73 &lt;DB&gt;

A:Cross-references: UNIPROT:P17495

A:Accession: C35982

A:Molecule type: protein

A:Residues: 1-72 &lt;DB2&gt;

C:Superfamily: disintegrin homology

C:Keywords: venom

F:1-73/Product: trigramin beta-2 #status experimental &lt;MA2&gt;

F:1-72/Product: trigramin beta-1 #status experimental &lt;MA1&gt;

F:1-72/Domain: disintegrin homology (fragment) &lt;DIS&gt;

F:51-53/Region: cell attachment (R-G-D) motif

Query Match 85.3%; Score 326; DB 2; Length 73;

Best Local Similarity 82.8%; Pred. No. 2.3e-25;

Matches 53; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 10 SPANPCDDATCTLTGSGCAGDLCCDCKFKMEGTVCRRARDDDDYCNGISAGCPRN 61

10 SPANPCDDATCTLTGSGCAGDLCCDCKFKMEGTVCRRARDDDDYCNGISAGCPRN 69

QY 62 PFHA 65

Db 70 PFHA 73

## RESULT 8

A30065

trigramin precursor - Indian green tree viper

N:Contains: hemorrhagic proteinase (EC 3.4.24.-); platelet aggregation inhibitor (distinct

C:Species: Trimeresurus gramineus (Indian green tree viper)

C&gt;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004

C:Accession: S12589; A30065; A29784

R:Nepper, M.P.; Jacobson, M.A.

Nucleic Acids Res. 18, 4255, 1990

A&gt;Title: Sequence of a cDNA encoding the platelet aggregation inhibitor trigramin.

A:Reference number: S12589; MUID:90352429; PMID:2377470

A:Accession: S12589

A:Molecule type: mRNA

A:Residues: 1-480 &lt;NEB&gt;

A:Cross-references: UNIPROT:P15503; EMBL:X51530; NID:964407; PIDN:CA35910.1; PID:964408

A:Note: translation of the signal sequence and the mature protein but not of the propept

R:huang, T.F.; Holt, J.C.; Kitzky, E.P.; Niewiarowski, S.

Biochemistry 28, 661-666, 1989

A&gt;Title: Trigramin: primary structure and its inhibition of von Willebrand factor bindin

A:Reference number: A30065; MUID:89229063; PMID:2653425

A:Accession: A30065

A:Molecule type: protein

A:Residues: 408-479 &lt;HUN&gt;

R:huang, T.F.; Holt, J.C.; Lukasiewicz, H.; Niewiarowski, S.

J. Biol. Chem. 262, 16157-16163, 1987

A&gt;Title: Trigramin. A low molecular weight peptide inhibiting fibrinogen interaction wit

A:Reference number: A29784; MUID:88058981; PMID:3680247

A:Accession: A29784

A:Molecule type: protein

A:Residues: 408-419 &lt;HUN&gt;

C:Superfamily: trigramin precursor; disintegrin homology

C:Keywords: anticoagulant; glycoprotein; hydrolase; metalloproteinase; venom; zinc; zymd

F:1-18/Domain: signal sequence #status predicted &lt;SIG&gt;

F:398-476/Domain: disintegrin homology &lt;DIS&gt;

F:408-479/Product: trigramin #status experimental &lt;MAT&gt;

F:458-460/Region: cell attachment (R-G-D) motif

F:279/Binding site: carboxylate (Asn) (covalent) #status predicted

F:333,337,343/Binding site: zinc (His) #status predicted

F:334/Active site: Glu #status predicted

Query Match 84.3%; Score 322; DB 1; Length 480;

Best Local Similarity 82.8%; Pred. No. 2.8e-24;

Matches 53; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 417 SPANPCDDATCTLTGSGCAGDLCCDCKFKMEGTVCRRARDDDDYCNGISAGCPRN 61

417 SPANPCDDATCTLTGSGCAGDLCCDCKFKMEGTVCRRARDDDDYCNGISAGCPRN 476

QY 62 PFHA 65

Db 477 PFHA 480

## RESULT 9

A33990

aplaggin - eastern cottonmouth

C:Species: Agkistrodon piscivorus piscivorus (eastern cottonmouth)

C&gt;Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 09-Jul-2004

C:Accession: A33990

R:Chao, B.H.; Jakubowski, J.A.; Savage, B.; Chow, E.P.; Marec, U.M.; Harker, L.A.; Mar

Proc. Natl. Acad. Sci. U.S.A. 86, 8050-8054, 1989

A&gt;Title: Agkistrodon piscivorus piscivorus platelet aggregation inhibitor: a potent inh

A:Reference number: A33990; MUID:90046735; PMID:2510158

A:Accession: A33990

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-71 &lt;CHA&gt;

A:Cross-references: UNIPROT:P16338

C:Superfamily: unassigned disintegrins; disintegrin homology

F:1-68/Domain: disintegrin homology (fragment) &lt;DIS&gt;

Query Match 84.2%; Score 321.5; DB 2; Length 71;

Best Local Similarity 85.7%; Pred. No. 7.8e-25;

Matches 54; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 2 APANPCDDATCTLTGSGCAGDLCCDCKFKMEGTVCRRARDDDDYCNGISAGCPRN 61

Db 10 SPANPCDDATCTLTGSGCAGDLCCDCKFKMEGTVCRRARDDDDYCNGISAGCPRN 68

QY 62 PFH 64

Db 69 PFH 71

## RESULT 10

G43019

platelet aggregation disintegrin (viridin), venom - prairie rattlesnake

C:Species: Crotalus viridis viridis (prairie rattlesnake)

C&gt;Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Aug-2004

C:Accession: G43019

R:Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten,

J. Biol. Chem. 268, 1058-1065, 1993

A&gt;Title: Characterization of the integrin specificities of disintegrins isolated from A

A:Reference number: A43019; MUID:93123215; PMID:8419314

A:Accession: G43019

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-71 &lt;SCA&gt;

A:Cross-references: UNIPROT:P1987

C:Superfamily: disintegrin homology

F:2-68/Domain: disintegrin homology &lt;DIS&gt;

Query Match 74.9%; Score 286; DB 2; Length 71;

Best Local Similarity 74.6%; Pred. No. 2.3e-21;

Matches 47; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

```

QY      2  APANPCDDAATCTKLTTSSQCADGICCDQCKFMKEGTVCRARGDDLDYDNGISAGCPRN 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      9  SPANPCDDAATCTKLTPGAQCADGICCDQCRFIKKGKICRRARGDDPDDRCTGQSADCPRN 68

```

QY	62 PFH 64
Db	69 RFH 71

## RESULT 11

platelet aggregation disintegrin (basilichn). venom - Mexican West-Coast rattlesnake  
 C:Species: Crocotalus basiliscus basiliscus (Mexican West-Coast rattlesnake)  
 C:Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Aug-2004  
 C:Accession: 143019  
 R:Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 1993  
 A:Title: Characterization of the integrin specificities of disintegrins isolated from An  
 A:Reference numbers: A43019, MUID:93123215, PMID:8419314  
 A:Accession: 143019  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-72 <SCA>  
 A:Cross-references: UNIPROT:P31981  
 C:Superfamily: disintegrin homology  
 /2-68/Domain: disintegrin homology <DIS>

Query Match	74.9%;	Score 286;	DB 2;	Length 72;
Best Local Similarity	73.4%;	Pred. No. 2.3e-21;		
Matches 47;	Conservative 8;	Mismatches 9;	Indels 0;	Gaps 0;

```
Qy      2 APANPCDDAATCKLTITTSQCADGICCCDCKCFMKSGTVCRARAGDDLDDYCIGISACPRN   61
          :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     9 SPANPCDDAATCKLRPGAQCAEGICCDQCRFIKKGKICRRARGDPDDRCTQGSAQCPRN   68
```

QY	62	PFHA	65
Db	69	HFHA	72

## RESULT 12

P:platelet aggregation disintegrin (molossin), venom - Northern blacktail rattlesnake  
 C:Species: Crocotalus molossus molossus (Northern blacktail rattlesnake)  
 C:Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Aug-2004  
 C:Accession: A43019  
 R:Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Namtizi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 1993  
 A:Title: Characterization of the integrin specificities of disintegrins isolated from A.  
 A:Reference number: A43019, MUID:93123215, PMID:8419314  
 A:Accession: A43019  
 A:Status: Preliminary  
 A:Molecule type: Protein  
 A:Residues: 1-73 <SCA>  
 A:Cross-references: UNIPROT:P31984  
 C:Superfamily: disintegrin homology  
 I:3-69/Domain: disintegrin homology <DIS>

Query Match	74.6%	Score 285;	DB 2;	Length 73;
Best Local Similarity	73.4%	Pred. No. 2.9e-21;		
Matches 47;	Conservative 7;	Mismatches 10;	Indels 0;	Gaps 0;

```

QY      2  APANPCDDAATCKLTTTSGCADGLCCDCKFMKEGTVCRARGBDDLDYCNGISAGCPRN 61
      :  |||||  :  |||||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB     10  SPENPCDDAATCKLRPGAQCADGLCCDQCRFIKKGKICRRARGDNPDRCYGSADCPRN 69

```

QY	62	PFHA	65
Db	70	PFHA	73

## RESULT 13

B43020  
platelet aggregation disintegrin (cereberin), venom - Arizona black rattlesnake  
C.Species: *Crotalus viridis cerberus* (Arizona black rattlesnake)  
C.Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 09-Jul-2004

Query Match	73.8%	Score 282	DB 2	Length 72
Best Local Similarity	73.0%	Pred. No. 5.7e-21		
Matches	46	Conservative	8	Mismatches 9
				Indels 0
				Gaps

```

QY      2  APANCCDAATCKLTGSGCADGLCCDQCKFMKEGTCRRARBDLDDYCNGISAGCPRN  61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      10 SPANCCDAATCKLTGAGCAEGLCCDQCRFTKKGKICRRARGDNPDDRCTGQADCPRN  69

```

QY	62 PFH 64
DB	70 RFH 72

RESULT 14

platelet aggregation disintegrin (lacthestin), venom - bushmaster  
C.Species: *Lachesis muta* (bushmaster)  
C.Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Aug-2004  
C.Accession: E43019  
R.Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arsten, J. Biol. Chem. 268, 1058-1065, 1993  
J.Title: Characterization of the integrin specificities of disintegrins isolated from *Am...*  
A.Reference number: A43019; MUID:93123215; PMID:8419314  
A.Accession: E43019  
A.Status: Preliminary  
A.Molecule type: protein  
A.Residues: 1-73 <SCA>  
A.Cross-references: UNIPROT:P31990  
C.Superfamily: disintegrin homology <DIS>  
F.3-69/Domain: disintegrin homology <DIS>

Query Match	72.3%;	Score 276;	DB 2;	Length 73;
Best Local Similarity	71.4%;	Pred. No. 2.2e-20;		
Matches 45; Conservative	9;	Mismatches 9;	Indels 0;	Gaps

```
Oy      2 APANCCDAATCKLTGSGCAGDLCCDQCFKFKEGTVCRARABDDLDYICNGISACGP RN   61  
        | :|::|||:::||::||::||::||::||  
Db       10 A PANCCDAATCKLRPGAGCGEGLCDQC R FKKGI CR ARAGEDNPDRC TGG SADCPR N   69
```

QY	62	PFH	64
		:::	
Db	70	GY	72

## RESULT 15

platelet aggregation disintegrin (tergeminin), venom - western massasauga  
CSpecies: *Sistrurus catenatus tergeminus* (western massasauga)  
CDate: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 09-Jul-2004  
CAccession: B40003  
RScarborough, R.M.; Rose, J.W.; Hsu, M.A.; Phillips, D.R.; Fried, V.A.; Campbell, A.M.;  
J. Biol. Chem. 266, 9359-9362, 1991  
ATitle: Barbourin, A GRP78- $\alpha$ -specific integrin antagonist from the venom of *Sistrurus*  
AReference number: A40003; MUID: 91236695; PMID: 2033037  
AAccession: B40003  
AStatus: Preliminary

A;Molecule type: protein  
 A;Residues: 1-73 <SCA>  
 A;Cross-references: UNIPROT:P22828  
 C;Superfamily: unassigned disintegrins; disintegrin homology  
 F;3-69/Domain: disintegrin homology <DIS>

Query Match 71.2%; Score 272; DB 2; Length 73;  
 Best Local Similarity 78.3%; Pred. No. 5.4e-20;  
 Matches 47; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 APANPCDDATCKLTGSGCAGDGLCCDQCKEMKEGTYCRRARGDDLDYCNGISAGCPRN 61  
 :|||||  
 Db 10 SPANPCDDATCKLRPGAGCAGDGLCCDQCKRFRKKGTVCRVARGDWNDTCTGQADCPRN 69  
 :|||||

Search completed: November 3, 2005, 08:19:35  
 Job time : 40 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 3, 2005, 08:10:02 ; Search time 177 Seconds

(Without alignments)  
188.052 Million cell updates/sec

Title: US-10-712-584-2\_COPY\_419\_483

Perfect score: 382  
Sequence: 1 DAPANPCCDATCKLTTSQ.....DLDDYCNISAGCPRNPFHA 65

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382	100.0	483	1	DISB_AGKCO
2	382	100.0	483	1	DISB_AGKCO
3	364	95.3	483	1	DISB_AGKPI
4	346	90.6	105	2	Q78CF2
5	346	90.6	317	2	Q90WC0
6	345	90.3	73	2	Q9DGH6
7	345	90.3	117	2	Q90D21
8	345	90.3	482	2	Q9PVK9
9	342	89.5	505	2	Q73795
10	340	89.0	477	2	Q98SP2
11	339	88.7	73	2	Q78ZD5
12	336	88.7	478	2	Q78ZD9
13	336	88.0	77	2	Q801Z4
14	336	88.0	484	1	DISB_TRJUE
15	334	87.4	73	1	DISG_TRIAB
16	334	87.4	73	1	DISG_TRIAB
17	333	87.2	89	2	Q698K8
18	333	85.3	480	2	Q90220
19	336	85.3	73	1	DISB_TRIGA
20	334	84.8	481	1	DIS2_TRIEL
21	323	84.6	488	2	Q8AMX7
22	322	84.3	480	1	DISA_TRIGA
23	321.5	84.0	71	1	DISI_AGKPI
24	321	84.0	71	1	DISI_AGKHA
25	291	76.2	71	2	Q9YH68
26	291	76.2	466	2	Q9YH68
27	291	76.2	479	2	Q9PW78
28	291	76.2	479	2	Q9PW78
29	290	75.9	476	2	Q9Y119
30	287	75.1	73	2	Q78ZD6
31	287	75.1	466	2	Q91MX6

32	287	75.1	483	2	Q78ZEO	Q78ZEO
33	286	74.9	71	1	DISI_CROV	P31987 crocalus v1
34	286	74.9	72	1	DISI_CROB	P31987 crocalus ba
35	285	74.6	73	1	DISI_CROM	P31984 crocalus mo
36	282	73.8	72	1	DISI_CROV	P31985 crocalus mu
37	276	72.3	73	1	DISI_IACMU	P31990 lachesis mu
38	275	72.0	108	2	Q93516	Q93516 agkistrodon
39	273	71.5	243	2	Q78T13	Q78T13 bothrops ja
40	272	71.2	73	1	DISI_SISC	P22828 sistrurus c
41	270	70.7	73	1	DISI_BOTU	P31989 bothrops ja
42	269	70.4	72	1	DISI_BOTU	P31988 bothrops co
43	269	70.4	72	1	DISI_CROAT	P31980 crocalus at
44	268	70.2	73	1	DISI_CROV	P31986 crocalus vi
45	268	70.2	115	2	Q90222	Q90222 agkistrodon

#### ALIGNMENTS

RESULT 1

ID	DISB_AGKCO	STANDARD	PRT	483 AA
AC	Q805F6			
DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Zinc metalloproteinase acostatin beta precursor (EC 3.4.24.-)			
DE	[contains: Disintegrin acostatin beta]			
OS	Agkistrodon contortrix contortrix (Southern copperhead)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubridae; Viperidae; Crotalinae; Agkistrodon.			
OC	NCBI_TaxID=8713;			
OX	[1]			
RN	SEQUENCE FROM N.A., SEQUENCE OF 419-482, FUNCTION, COFACTOR, AND			
RP	SUBUNIT.			
RC	TISSUE=Venom;			
RX	PubMed=12450389; DOI=10.1021/bj025876s;			
RA	Okuda D., Koike H., Morita T.;			
RT	"A new gene structure of the disintegrin family: a subunit of dimeric			
RL	disintegrin has a short coding region.";			
RL	Biochemistry 41:14248-14254(2002).			
CC	-1- FUNCTION: The metalloproteinase is a probable venom zinc protease			
CC	that acts in hemorrhage (By similarity).			
CC	-1- FUNCTION: Acostatin inhibits fibrinogen interaction with platelet			
CC	receptors expressed on glycoprotein IIb-IIIa complex. Acts by			
CC	binding to the glycoprotein IIb-IIIa receptor on the platelet			
CC	surface and inhibits ADP-induced platelet aggregation in human			
CC	platelet-rich plasma.			
CC	-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).			
CC	-1- SUBUNIT: Acostatin is a heterodimer of an alpha and a beta			
CC	subunit.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Expressed by the venom gland.			
CC	-1- SIMILARITY: Belongs to the peptidase M12B family.			
CC	-1- SIMILARITY: Contains 1 disintegrin domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
DR	EMBL; AB078904; BAC55945.1; -			
DR	HSSP; P15167; IDTH.			
DR	InterPro; IPR001762; Disintegrin.			
DR	InterPro; IPR006025; Pept_M_Zn_BS.			
DR	InterPro; IPR001590; Peptidase_M12B.			
DR	InterPro; IPR002870; Peptidase_M12B_N.			
DR	Pfam; PF00200; Disintegrin; 1.			
DR	Pfam; PF01562; Pep_M12B_propep; 1.			

```
DR Pfam: PF01421; Reprolysin; 1.
DR PRINTS: PR00289; Disintegrin; 1.
DR ProDom: PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Blood coagulation; Cell adhesion; Direct protein sequencing;
KW Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 20
FT PROPEP 191
FT CHAIN 192 334
FT PROPEP 395 418
FT CHAIN 419 483
FT DOMAIN 198 394
FT DOMAIN 402 482
FT SITE 461 463
FT METAL 334 335
FT ACT SITE 335 335
FT METAL 338 338
FT METAL 344 344
FT DISULFID 309 389
FT DISULFID 349 356
FT DISULFID 425 448
FT DISULFID 426 426
FT DISULFID 431 431
FT DISULFID 439 445
FT DISULFID 444 469
FT DISULFID 457 476
SQ SEQUENCE 483 AA; 54025 MW; 6D91926570971221 CRC64;

Query Match
Best Local Similarity 100.0%; Score 382; DB 1; Length 483;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAPANPCDAATCKLTGSGCADGLCCDCKFMKEGTVCRRARGLDLDYCNIGISAGCR 60
DB 419 DAPANPCDAATCKLTGSGCADGLCCDCKFMKEGTVCRRARGLDLDYCNIGISAGCR 478
OY 61 NPFHA 65
DB 479 NPFHA 483

RESULT 2
DISI_AGKCO STANDARD; PRT; 483 AA.
ID DISI_AGKCO
AC 09IAB0;
DT 05-JUL-2004 (Rel. 44, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Zinc metalloproteinase contortrostatin precursor (EC 3.4.24.-)
DE [Contains: Disintegrin contortrostatin].
OS Agkistrodon contortrix contortrix (Southern copperhead).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodermata; Squamata; Chordata; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=8713;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 419-433, FUNCTION, COFACTOR, AND
RP SUBUNIT.
RC TISSUE=Venom gland;
RX MEDLINE=20166949; PubMed=10700384; DOI=10.1006/abbi.1999.1682;
RA Zhou Q., Hu P., Rittner M.R., Swenson S.D., Argounova S., Epstein A.L.,
RA Markland F.S.;
RT "Molecular cloning and functional expression of contortrostatin, a
RT homodimeric disintegrin from southern copperhead snake venom.";
RL Arch. Biochem. Biophys. 375:278-288(2000).
CC -!- FUNCTION: The metalloproteinase is a probable venom zinc protease
CC that acts in hemorrhage (By similarity).
```

```
CC -!- FUNCTION: The disintegrin binds and inhibits integrins alpha-
CC Iib/beta-3, alpha-5/beta-1, alpha-V/beta-3, and alpha-V/beta-5. It
CC blocks cancer cell adhesion to fibronectin and vitronectin and
CC thus prevents invasion of cancer cells.
CC -!- COFACTOR: Binds 1 zinc ion per subunit.
CC -!- SUBUNIT: Homodimer; disulfide-linked (disintegrin).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the peptidase M12B family.
CC -!- SIMILARITY: Contains 1 disintegrin domain.
-----
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-----
CC EMBL; AF212305; AAF65171.1; -.
CC HSSP; P18619; 1FVL.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Blood coagulation; Cell adhesion; Direct protein sequencing;
KW Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 20
FT PROPEP 191 190
FT CHAIN 191 394
FT PROPEP 395 418
FT CHAIN 419 483
FT DOMAIN 198 394
FT DOMAIN 402 482
FT SITE 461 463
FT METAL 334 334
FT METAL 335 335
FT ACT SITE 338 338
FT METAL 344 344
FT DISULFID 309 389
FT DISULFID 349 356
FT DISULFID 425 448
FT DISULFID 439 445
FT DISULFID 444 469
FT DISULFID 457 476
SQ SEQUENCE 483 AA; 53948 MW; 2DBB370FDC590007 CRC64;

Query Match
Best Local Similarity 100.0%; Score 382; DB 1; Length 483;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAPANPCDAATCKLTGSGCADGLCCDCKFMKEGTVCRRARGLDLDYCNIGISAGCR 60
DB 419 DAPANPCDAATCKLTGSGCADGLCCDCKFMKEGTVCRRARGLDLDYCNIGISAGCR 478
OY 61 NPFHA 65
DB 479 NPFHA 483

RESULT 3
DISB_AGKPI STANDARD; PRT; 483 AA.
ID DISB_AGKPI
```



AC Q805F4; 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Zinc metalloproteinase piscivostatin beta precursor (EC 3.4.24.-)  
 DE [contains: Disintegrin piscivostatin beta]  
 OS Agkistrodon piscivorus piscivorus (Basen cottonmouth).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Agkistrodon.  
 NC NCBI\_TaxID=8716;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SUBUNIT.  
 RC TISSUE=Venom;  
 RX PubMed=12450389; DOI=10.1021/bi025876s;  
 RA Okuda D., Koike H., Morita T.;  
 RT "A new gene structure of the disintegrin family: a subunit of dimeric  
 RT disintegrin has a short coding region.";  
 RL Biochemistry 41:14248-14254(2002).  
 RP SEQUENCE OF 415-483, AND CHARACTERIZATION OF PISCIVOSTATIN BETA.  
 RC TISSUE=Venom;  
 RX PubMed=11530017;  
 RA Okuda D., Morita T.;  
 RT "Purification and characterization of a new RGD/KGD-containing dimeric  
 RT disintegrin, piscivostatin, from the venom of Agkistrodon piscivorus  
 RT piscivorus: the unique effect of piscivostatin on platelet  
 RT aggregation.";  
 RL J. Biochem. 130:407-415(2001).  
 CC -1- FUNCTION: The metalloproteinase is a probable venom zinc protease  
 CC that acts in hemostasis (By similarity).  
 CC -1- FUNCTION: Piscivostatin inhibits fibrinogen interaction with  
 CC platelet receptors expressed on glycoprotein IIb-IIIa complex.  
 CC Acts by binding to the glycoprotein IIb-IIIa receptor on the  
 CC platelet surface and inhibits both ADP-induced platelet  
 CC aggregation and platelet aggregate dissociation in human platelet-  
 CC rich plasma.  
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -1- SUBUNIT: Piscivostatin is a heterodimer of an alpha and a beta  
 CC subunit.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -1- SIMILARITY: Belongs to the peptidase M12B family.  
 CC -1- SIMILARITY: Contains 1 disintegrin domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL AB078906; BAC55947.1; -  
 DR HSSP; P15167; IDTH.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR006025; Pept M Zn BS.  
 DR InterPro: IPR001590; Peptidase\_M12B.  
 DR InterPro: IPR002870; Peptidase\_M12B\_N.  
 DR Pfam; PF00200; Disintegrin; 1.  
 DR Pfam; PF01562; Pept\_M12B\_propep; 1.  
 DR Pfam; PF01421; Reprolysin; 1.  
 DR PRINTS; PR00289; DISINTEGRIN.  
 DR ProDom; PD000664; Disintegrin; 1.  
 DR SMART; SM00050; DISIN; 1.  
 DR PROSITE; PS50215; ADAM\_MEPRO; 1.  
 DR PROSITE; PS00427; DISINTEGRIN\_1; FALSE\_NEG.  
 DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KW Blood coagulation; Cell adhesion; Direct protein sequencing;  
 KW Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.  
 FT SIGNAL 1 20 Potential.  
 FT PROPEP 21 191 Potential.

FT CHAIN 192 394 Zinc metalloproteinase piscivostatin  
 FT PROPEP 395 414 Spacer peptide (Potential).  
 FT CHAIN 415 483 Disintegrin piscivostatin beta.  
 FT DOMAIN 198 394 Metalloprotease.  
 FT SITE 402 482 Disintegrin-like.  
 FT METAL 461 463 Cell attachment site (atypical).  
 FT ACT SITE 334 334 Zinc (catalytic).  
 FT METAL 335 335 Zinc (catalytic).  
 FT METAL 338 338 Zinc (catalytic).  
 FT METAL 344 344 Zinc (catalytic).  
 FT DISULFID 309 389 By similarity.  
 FT DISULFID 349 356 By similarity.  
 FT DISULFID 425 448 By similarity.  
 FT DISULFID 426 426 Interchain (with C-54 in alpha subunit)  
 FT DISULFID 431 431 (By similarity).  
 FT DISULFID 439 445 Interchain (with C-59 in alpha subunit)  
 FT DISULFID 444 469 (By similarity).  
 FT DISULFID 457 476 By similarity.  
 SQ SEQUENCE 483 AA; 54072 MW; F1DA9CEBF00DE3E7 CRC64;  
 Query Match 95.3%; Score 364; DB 1; Length 483;  
 Best Local Similarity 93.8%; Pred. No. 4.7e-31;  
 Matches 61; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DAPANPCCAATCKLTTSQCADGLCCDDCKFKKCTGVRARGDLDLYCNISAGCPR 60  
 DB 419 DAPANPCCAATCKLTTPSGCAEGLCCDDCKFKKCTGVRARGDLDLYCNISAGCPR 478  
 QY 61 NPFA 65  
 DB 479 NPFA 483  
 RESULT 4  
 ID 078CP2 PRELIMINARY; PRT; 105 AA.  
 AC 078CP2;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Platelet aggregation inhibitor disintegrin (Fragment).  
 GN Name=salmostin;  
 OS Agkistrodon halys brevicaudus (Korean slamosa snake) (Gloydius halys  
 OS brevicaudus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Gloydius.  
 NC NCBI\_TaxID=259325;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kang I.C., Chung K.H., Lee S.J., Yun Y.D., Moon H.M., Kim D.S.;  
 RT "Purification and molecular cloning of a platelet aggregation  
 RT inhibitor from the snake (Agkistrodon halys brevicaudus) venom.";  
 RL Thromb. Res. 0:0-0(1998).  
 DR EMBL AF054626; AAC08997.1; -  
 DR GO; GO:007229; P: integrin-mediated signaling pathway; IEA.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Peptidase\_M12B.  
 DR InterPro: IPR000519; P\_trefol-1.  
 DR Pfam; PF00200; Disintegrin; 1.  
 DR Pfam; PF01421; Reprolysin; 1.  
 DR PRINTS; PR00289; DISINTEGRIN.  
 DR PRINTS; PR00680; PTFREPOL.  
 DR ProDom; PD000664; Disintegrin; 1.  
 DR SMART; SM00050; DISIN; 1.  
 DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
 DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
 KW Integrin.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 105 AA; 11407 MW; 6F10AD4496D35F2 CRC64;



Fri Nov 4 10:27:40 2005

Best Local Similarity 87.5%; Pred. No. 1.5e-29;  
Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 APANPCDDATCTLTGSGCAGLCCDQCKFMKEGTVCRARAGDDDDYCNGISAGCPRN 61  
DB 54 APANPCDDATCTLTGSGCAGLCCDQCKFMKEGTVCRARAGDDDDYCNGISAGCPRN 113  
QY 62 PFHA 65  
DB 114 PFHA 117

## RESULT 8

Q9PVK9 PRELIMINARY; PRT; 482 AA.  
AC Q9PVK9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Metalloprotease.  
GN Name=Mt-d;  
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Gloydius.  
OX NCBI\_TaxID=8714;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=brevicaudus; TISSUE=Venom;  
RA MEDLINE=9337693; PubMed=10406963;  
RA Jeon O.H., Kim D.S.;  
RT "Molecular cloning and functional characterization of a snake venom metallopeptidase";  
RT Eur. J. Biochem. 263:526-533(1999).  
DR EMBL; AF051789; AAD02654.1; -.  
DR HSSP; P21859; 1J2L.  
DR GO; GO:0005840; C:intracellular; IEA.  
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
DR GO; GO:0006412; P:protein biosynthesis; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001762; Disintegrin.  
DR InterPro; IPR001590; Peptidase\_M12B.  
DR InterPro; IPR002870; Peptidase\_M12B\_N.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR001515; Ribosomal\_L32E.  
DR Pfam; PF00200; Disintegrin; 1.  
DR Pfam; PF01562; Pep\_M12B\_propep; 1.  
DR Pfam; PF01421; Repolysin; 1.  
DR PRINTS; PR00289; DISINTEGRIN.  
DR ProDom; PD000664; Disintegrin; 1.  
DR SMART; SM00050; DISIN; 1.  
DR PROSITE; PS50215; ADAM\_MERPRO; 1.  
DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
DR PROSITE; PS00214; DISINTEGRIN\_2; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Metalloprotease; Protease.  
SQ SEQUENCE 482 AA; 53409 MW; C6014BBE7BC8B15 CRC64;

Query Match 90.3%; Score 345; DB 2; Length 482;  
Best Local Similarity 87.5%; Pred. No. 5.2e-29;

Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 APANPCDDATCTLTGSGCAGLCCDQCKFMKEGTVCRARAGDDDDYCNGISAGCPRN 61  
DB 419 APANPCDDATCTLTGSGCAGLCCDQCKFMKEGTVCRARAGDDDDYCNGISAGCPRN 478

QY 62 PFHA 65  
DB 479 PFHA 482

## RESULT 9

Q73795 PRELIMINARY; PRT; 505 AA.  
AC Q73795;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Metalloprotease.  
GN Name=Mt-b;  
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Gloydius.  
OX NCBI\_TaxID=8714;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=brevicaudus; TISSUE=Venom;  
RA Jeon O.H., Kim D.S.;  
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF051788; AAD02653.1; -.  
DR HSSP; P21859; 1J2L.  
DR GO; GO:0005840; C:intracellular; IEA.  
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0005840; C:ribosome; IEA.  
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
DR GO; GO:0006412; P:protein biosynthesis; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001762; Disintegrin.  
DR InterPro; IPR001590; Peptidase\_M12B.  
DR InterPro; IPR002870; Peptidase\_M12B\_N.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR001515; Ribosomal\_L32E.  
DR Pfam; PF00200; Disintegrin; 1.  
DR Pfam; PF01562; Pep\_M12B\_propep; 1.  
DR Pfam; PF01421; Repolysin; 1.  
DR PRINTS; PR00289; DISINTEGRIN.  
DR ProDom; PD000664; Disintegrin; 1.  
DR SMART; SM00050; DISIN; 1.  
DR PROSITE; PS50215; ADAM\_MERPRO; 1.  
DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Metalloprotease; Protease.  
SQ SEQUENCE 505 AA; 56336 MW; C96B99FC9C05378F CRC64;

Query Match 89.5%; Score 342; DB 2; Length 505;  
Best Local Similarity 85.9%; Pred. No. 1.1e-28;

Matches 55; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 APANPCDDATCTLTGSGCAGLCCDQCKFMKEGTVCRARAGDDDDYCNGISAGCPRN 61  
DB 442 APANPCDDATCTLTGSGCAGLCCDQCKFMKEGTVCRARAGDDDDYCNGISAGCPRN 501

QY 62 PFHA 65  
DB 502 PFHA 505

## RESULT 10

Q98SP2 PRELIMINARY; PRT; 477 AA.  
AC Q98SP2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Bothrops jararaca.  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Silva C.A., Martins de Camargo A.C., de Toledo Serrano S.M.;  
RL Submitted (FEF-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF345931; AAK15542.1; -  
DR HSSP: P21859; 1J2L.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0005840; C:ribosome; IEA.  
DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.  
DR GO: GO:0006412; P:protein biosynthesis; IEA.  
DR GO: GO:0005508; P:protein biosynthesis and peptidolysis; IEA.  
DR InterPro: IPR001762; Disintegrin.  
DR InterPro: IPR001590; Peptidase\_M12B.  
DR InterPro: IPR002870; Peptidase\_M12B\_N.  
DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
DR Pfam: PF00200; Disintegrin; 1.  
DR Pfam: PF01562; Pep\_M12B\_propep; 1.  
DR Pfam: PF01421; Reprolysin; 1.  
DR PRINTS: PR00289; DISINTEGRIN.  
DR ProDom: PD000664; Disintegrin; 1.  
DR SMART: SM00050; DISIN; 1.  
DR PROSITE: PS50215; ADAM\_MEPRO; 1.  
DR PROSITE: PS00427; DISINTEGRIN\_1; 1.  
DR PROSITE: PS00142; DISINTEGRIN\_2; 1.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
RN SEQUENCE 477 AA; 53440 MW; AC973EE767E10B3 CRC64;  
SQ

Query Match 89.0%; Score 340; DB 2; Length 477;

Best Local Similarity 87.3%; Pred. No. 1,8e-28; Matches 55; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PANPCCDAATCKLTTSQCADGLCCDQCKFMKEGTVCRARGGDLDLYCNGISAGCPR 62  
DB 415 PGNPCCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVCRARGGDMDYCNGISAGCPR 474  
QY 63 PFA 65  
DB 475 PFA 477

RESULT 11  
ID 07SZD5 PRELIMINARY; PRT; 73 AA.  
AC 07SZD5;  
DT 01-OCT-2003 (TEMBLrel. 25, Created)  
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
DE Disintegrin (Fragment).  
OS Agkistrodon caliginosus (Korean viper) (Gloydus ussuriensis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Gloydus.  
OX NCBT\_TaxID=35671;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Snake venom gland;  
RA Sun D.-Y., Yang T.-S.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY204245; AAP20644.1; -  
DR HSSP: P21859; 1J2L.  
DR GO: GO:0007229; P:integrin-mediated signaling pathway; IEA.  
DR InterPro: IPR001762; Disintegrin.  
DR Pfam: PF00200; Disintegrin; 1.  
DR ProDom: PD000664; Disintegrin; 1.  
DR SMART: SM00050; DISIN; 1.  
DR PROSITE: PS00427; DISINTEGRIN\_1; 1.  
DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
KW Integrin.  
FT NON TER 1 1  
SQ SEQUENCE 73 AA; 7768 MW; 615509DF966882EF CRC64;

Query Match 88.7%; Score 339; DB 2; Length 73;  
Best Local Similarity 84.6%; Pred. No. 4,5e-29;  
Matches 55; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAPANPCCDAATCKLTTSQCADGLCCDQCKFMKEGTVCRARGGDLDLYCNGISAGCPR 60  
DB 9 DSNPCCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVCRARGGDMDYCNGISAGCPR 68  
QY 61 NPFA 65  
DB 69 NPFA 73

RESULT 12  
ID 07SZD9 PRELIMINARY; PRT; 478 AA.  
AC 07SZD9;  
DT 01-OCT-2003 (TEMBLrel. 25, Created)  
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
DE Metalloprotease/disintegrin ussuri.  
OS Agkistrodon caliginosus (Korean viper) (Gloydus ussuriensis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Gloydus.  
OX NCBT\_TaxID=35671;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Snake venom gland;  
RA Sun D.-Y., Yang T.-S.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY204245; AAP20644.1; -  
DR HSSP: P21859; 1J2L.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0005840; C:ribosome; IEA.  
DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.  
DR GO: GO:0007229; P:integrin-mediated signaling pathway; IEA.  
DR GO: GO:0006412; P:protein biosynthesis; IEA.  
DR GO: GO:0005508; P:protein biosynthesis and peptidolysis; IEA.  
DR InterPro: IPR001762; Disintegrin.  
DR InterPro: IPR001590; Peptidase\_M12B.  
DR InterPro: IPR002870; Peptidase\_M12B\_N.  
DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro: IPR001515; Ribosomal\_L32E.  
DR Pfam: PF00200; Disintegrin; 1.  
DR Pfam: PF01562; Pep\_M12B\_propep; 1.  
DR Pfam: PF01421; Reprolysin; 1.  
DR ProDom: PD000664; Disintegrin; 1.  
DR SMART: SM00050; DISIN; 1.  
DR PROSITE: PS50215; ADAM\_MEPRO; 1.  
DR PROSITE: PS00427; DISINTEGRIN\_1; 1.  
DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Integrin.  
SQ SEQUENCE 478 AA; 53443 MW; CD2FBC975F62A771 CRC64;

Query Match 88.7%; Score 339; DB 2; Length 478;

Best Local Similarity 84.6%; Pred. No. 2,3e-28; Matches 55; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAPANPCCDAATCKLTTSQCADGLCCDQCKFMKEGTVCRARGGDLDLYCNGISAGCPR 60  
DB 414 DSNPCCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVCRARGGDMDYCNGISAGCPR 473  
QY 61 NPFA 65  
DB 474 NPFA 478

RESULT 13  
ID 080124 PRELIMINARY; PRT; 77 AA.

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AC Q80124;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Disintegrin (Fragment).
OS Bothrops alternatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
NCBI_TaxID=64174;
RN [1]
RP SEQUENCE FROM N.A.
RA Ramos O.H.P., Sellastre-de-Araujo H.S.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY259516; AAO75107.1; -.
DR HSSP; P21859; 1J2L.
DR GO; GO:0007229; P: integrin-mediated signaling pathway; IEA.
DR InterPro; IPR001762; Disintegrin.
DR Pfam; PF00200; Disintegrin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
KW Integrin.
FT NON TER
SQ SEQUENCE 77 AA; 8179 MW; 680501C26E7ED496 CRC64;

Query Match 88.0%; Score 336; DB 2; Length 77;
Best Local Similarity 87.3%; Pred. No. 9.9e-29;
Matches 55; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PNPCCDAATCKLTTSQCADGLCCDQCFMKKGTGCRARGGDDLDYCNGISAGCPNPP 62
DB 15 PNPCCDAATCKLTTSQCADGLCCDQCFMKKGTGCRARGGDDLDYCNGISAGCPNPP 74

QY 63 FHA 65
DB 75 FHA 77

RESULT 14
DIST TRIJE STANDARD; PRT; 484 AA.
AC P63912;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Zinc metalloproteinase jerdonitin precursor (EC 3.4.24.-) [Contains:
DE Disintegrin jerdonitin].
OS Trimeresurus jerdoniti (Jerdon's pit-viper) (Protobothrops jerdoni).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Trimeresurus.
NCBI_TaxID=135726;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 206-214; 221-233; 299-308;
RP 310-344; 451-453 AND 460-484.
RC TISSUE=Venom;
RA MEDLINE=22873278; PubMed=14511668; DOI=10.1016/j.bjrc.2003.09.009;
RA Chen R.-Q., Jin Y., Wu J.-B., Zhou X.-D., Lu Q.-M., Wang W.-Y.,
RA Xiong Y.-L.;
RA "A new protein structure of P-II class snake venom metalloproteinases:
RT it comprises metalloproteinase and disintegrin domains.";
RL Biochem. Biophys. Res. Commun. 310:182-187(2003).
CC -1- FUNCTION: The metalloproteinase is a probable venom zinc protease
CC that acts in hemorrhage (By similarity).
CC -1- FUNCTION: jerdonitin inhibits fibrinogen interaction with platelet
CC receptors expressed on glycoprotein IIb-IIIa complex. Acts by
CC binding to the glycoprotein IIb-IIIa receptor on the platelet
CC surface and inhibits aggregation induced by ADP, thrombin,
CC platelet-activating factor and collagen (By similarity).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

```

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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the peptidase M12B family.
CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY64231; AA063966.1; -.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
KW Blood coagulation; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 20
FT PROPEP 21 191
FT CHAIN 192 392
FT PROPEP 393 410
FT CHAIN 411 484
FT SITE 462 464
FT METAL 330 330
FT ACT SITE 331 331
FT METAL 334 334
FT METAL 340 340
FT METAL 340 340
FT DISULFID 305 387
FT DISULFID 347 352
FT DISULFID 403 422
FT DISULFID 414 432
FT DISULFID 416 427
FT DISULFID 426 449
FT DISULFID 440 449
FT DISULFID 440 470
FT DISULFID 445 477
FT DISULFID 458 477
SQ SEQUENCE 484 AA; 54613 MW; 8D603EE7C0F48232 CRC64;

Query Match 88.0%; Score 336; DB 1; Length 484;
Best Local Similarity 90.2%; Pred. No. 4.9e-28;
Matches 55; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 NPPCCDAATCKLTTSQCADGLCCDQCFMKKGTGCRARGGDDLDYCNGISAGCPNPP 64
DB 424 NPPCCDAATCKLTTSQCADGLCCDQCFMKKGTGCRARGGDDLDYCNGISAGCPNPP 483

QY 65 A 65
DB 484 A 484

RESULT 15
DIST TRIAB STANDARD; PRT; 73 AA.
AC P62384;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Disintegrin albolabrin (Platelet aggregation activation inhibitor).
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Trimeresurus.  
OX NCB1\_TaxID=8765;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Venom;  
RX MEDLINE=90283463; PubMed=2191722; DOI=10.1016/0167-4838(90)90229-9;  
RA Williams J., Rucinski B., Holt J., Niewiarowski S.;  
RT "Elegantin and albolabrin purified peptides from viper venoms:  
RT homologues with the RGDs domain of fibrinogen and von Willebrand  
RT factor.";  
RL Biochim. Biophys. Acta 1039:81-89(1990).

RN [2]  
RP DISULFIDE BONDS.

RC TISSUE=Venom;  
RX MEDLINE=91242430; PubMed=2036389;  
RA Calvete J.J., Schaefer W., Soszka T., Lu W., Cook J.J., Jameson B.A.,  
RA Niewiarowski S.;  
RT "Identification of the disulfide bond pattern in albolabrin, an RGD-  
RT containing peptide from the venom of Trimeresurus albolabris:  
RT significance for the expression of platelet aggregation inhibitory  
RT activity.";  
RL Biochemistry 30:5225-5229(1991).

RN [3]  
RP STRUCTURE BY NMR.

RX MEDLINE=94109384; PubMed=8281937;  
RA Jasela M., Smith K.J., Lu X., Williams J.A., Trayer H., Trayer I.P.,  
RA Hyde E.I.;  
RT "1H-NMR studies and secondary structure of the RGD-containing snake  
RT toxin, albolabrin.";  
RL Eur. J. Biochem. 218:853-860(1993).

RN [4]  
RP STRUCTURE BY NMR.

RX MEDLINE=97052455; PubMed=8697089;  
RA Smith K.J., Jasela M., Lu X., Williams J.A., Hyde E.I., Trayer I.P.;  
RT "Three-dimensional structure of the RGD-containing snake toxin  
RT albolabrin in solution, based on 1H NMR spectroscopy and simulated  
RT annealing calculations.";  
RL Int. J. Pept. Protein Res. 48:220-228(1996).

-I- FUNCTION: Inhibits fibrinogen interaction with platelet receptors  
expressed on glycoprotein IIb-IIIa complex. Acts by binding to the  
glycoprotein IIb-IIIa receptor on the platelet surface and  
inhibits aggregation induced by ADP, thrombin, platelet-activating  
factor and collagen.

CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -I- SIMILARITY: Belongs to the disintegrin family.

DR PIR; A23731; A23731.

DR HSP; P18619; IFLV.

DR InterPro; IPR001762; Disintegrin.

DR Pfam; PF00200; Disintegrin; 1.

DR PRINTS; PR00289; DISINTEGRIN.

DR ProDom; PD000664; Disintegrin; 1.

DR SMART; SM00050; DISIN; 1.

DR PROSITE; PS00427; DISINTEGRIN\_1; 1.

DR PROSITE; PS50214; DISINTEGRIN\_2; 1.

KW Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.

FT DISULFID 6 15 Probable.

FT DISULFID 8 16 Probable.

FT DISULFID 21 35 Probable.

FT DISULFID 29 59 Probable.

FT DISULFID 34 38 Probable.

FT DISULFID 47 66 Probable.

FT SITE 51 53 Cell attachment site.

FT SITE 73 73 AA; 7573 MW; F7E011E2F46FEF14 CRC64;

Query Match 87.4%; Score 334; DB 1; Length 73;

Best Local Similarity 84.4%; Pred. No. 1.5e-28;

Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDAATCTLTGSCADGLCCDDCKFMKEGTVCRRARGGDLDYXNGISAGCPN 61

DB 10 SPANPCDAATCTLTGSCADGLCCDDCKFMKEGTVCRRARGGDLDYXNGISAGCPN 69

QY 62 PFA 65  
DB 70 PFA 73

Search completed: November 3, 2005, 08:18:51  
Job time : 179 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:13:22 ; Search time 42 Seconds  
(without alignments)  
115.528 Million cell updates/sec

Title: US-10-712-584-2\_COPY\_419\_483

Perfect score: 382

Sequence: 1 DAPANPCDDATCKLTGSGQCADGICCDQCKFMKEGTVCRARAGDLDLYCNGISAGCPR 65

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUTS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	382	100.0	483	4	US-09-460-295B-2
2	337	88.2	72	6	5182260-21
3	337	88.2	72	6	5182260-21
4	337	88.2	73	6	5182260-2
5	337	88.2	73	6	5182260-2
6	334	87.4	73	1	US-07-965-674-14
7	334	87.4	73	4	US-08-993-165-15
8	334	87.4	73	4	US-09-243-640-13
9	334	87.4	73	4	US-08-929-847-15
10	334	87.4	73	4	US-09-460-295B-9
11	334	87.4	73	4	US-09-813-484-15
12	334	87.4	73	5	PCT-US93-09523-14
13	332	86.9	73	4	US-09-776-268A-1
14	329	86.1	73	4	US-09-540-448-15
15	329	86.1	73	4	US-10-046-801-15
16	325	85.1	99	1	US-07-623-611-5
17	325	85.1	99	1	US-07-623-611-8
18	325	85.1	99	5	PCT-US91-09108-5
19	325	85.1	99	5	PCT-US91-09108-8
20	325	85.1	106	1	US-07-623-611-4
21	325	85.1	106	5	US-07-623-611-7
22	325	85.1	106	5	PCT-US91-09108-4
23	325	85.1	106	5	PCT-US91-09108-7
24	323.5	84.7	71	1	US-07-602-847C-24
25	322	84.3	98	1	US-07-623-611-6
26	322	84.3	98	1	US-07-623-611-9
27	322	84.3	98	5	PCT-US91-09108-6

28	322	84.3	98	5	PCT-US91-09108-9	Sequence 9, Appl1
29	322	84.3	552	4	US-09-460-295B-8	Sequence 8, Appl1
30	321.5	84.2	71	1	US-07-965-674-10	Sequence 10, Appl1
31	321.5	84.2	71	4	US-09-460-295B-7	Sequence 7, Appl1
32	321.5	84.2	71	5	PCT-US93-09523-10	Sequence 10, Appl1
33	319	83.5	72	1	US-07-623-611-1	Sequence 1, Appl1
34	319	83.5	72	5	PCT-US91-09108-1	Sequence 2, Appl1
35	319	83.5	96	1	US-07-623-611-2	Sequence 3, Appl1
36	319	83.5	96	1	US-07-623-611-3	Sequence 2, Appl1
37	319	83.5	96	5	PCT-US91-09108-2	Sequence 3, Appl1
38	319	83.5	96	5	PCT-US91-09108-3	Sequence 3, Appl1
39	318	83.2	72	1	US-07-602-847C-23	Sequence 23, Appl1
40	307.5	80.5	73	1	US-07-965-674-5	Sequence 5, Appl1
41	307.5	80.5	73	5	PCT-US93-09523-5	Sequence 5, Appl1
42	293.5	76.8	71	6	5318899-17	Patent No. 5318899
43	293.5	76.8	71	6	5318899-17	Patent No. 5318899
44	286	74.9	71	6	5318899-11	Patent No. 5318899
45	286	74.9	71	6	5318899-11	Patent No. 5318899

#### ALIGNMENTS

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RESULT 1
US-09-460-295B-2
; Sequence 2, Application US/09460295B
; Patent No. 6710030
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; FILE REFERENCE: 1279-3383/09801388
; CURRENT APPLICATION NUMBER: US/09/460,295B
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/163,047
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Agkistrodon contortrix
US-09-460-295B-2

Query Match      100.0%; Score 382; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.3e-30; Indels 0; Gaps 0;
Matches 65; Conservative 0; Mismatches 0;

QY      1 DAPANPCDDATCKLTGSGQCADGICCDQCKFMKEGTVCRARAGDLDLYCNGISAGCPR 60
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DB      419 DAPANPCDDATCKLTGSGQCADGICCDQCKFMKEGTVCRARAGDLDLYCNGISAGCPR 478

QY      61 NEFHA 65
      |||
DB      479 NEFHA 483

RESULT 2
5182260-21
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
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;SEQ ID NO:21:
; LENGTH: 72
5182260-21

Query Match
Best Local Similarity 88.2%; Score 337; DB 6; Length 72;
Matches 55; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLTTGSCADGLCCDQCKFMKEGTVCRARGDDLDDYCNGISAGCPRN 61
Db 10 SPENPCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVCRARGDNDVNDYCNGISAGCPRN 69

Qy 62 PFH 64
Db 70 PFH 72

RESULT 3
5182260-21
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:21:
; LENGTH: 72
5182260-21

Query Match
Best Local Similarity 88.2%; Score 337; DB 6; Length 72;
Matches 55; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLTTGSCADGLCCDQCKFMKEGTVCRARGDDLDDYCNGISAGCPRN 61
Db 10 SPENPCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVCRARGDNDVNDYCNGISAGCPRN 69

Qy 62 PFH 64
Db 70 PFH 72

RESULT 4
5182260-2
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:2:
; LENGTH:73
5182260-2

Query Match
Best Local Similarity 88.2%; Score 337; DB 6; Length 73;
Matches 55; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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Qy 62 PFH 64
Db 71 PFH 73

RESULT 5
5182260-2
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:2:
; LENGTH:73
5182260-2

Query Match
Best Local Similarity 88.2%; Score 337; DB 6; Length 73;
Matches 55; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLTTGSCADGLCCDQCKFMKEGTVCRARGDDLDDYCNGISAGCPRN 61
Db 11 SPENPCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVCRARGDNDVNDYCNGISAGCPRN 70

Qy 62 PFH 64
Db 71 PFH 73

RESULT 6
US-07-965-674-14
; Sequence 14, Application US/07965674
; Patent No. 5380646
; GENERAL INFORMATION:
; APPLICANT: Knight, Linda C.
; TITLE OF INVENTION: Thrombus Detection Using
; TITLE OF INVENTION: Radiolabelled Dintegrins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Temple University - Of The Common-
; ADDRESSES: wealth System Of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/965,674
; FILING DATE: 19921019
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```



```

? NAME: Monaco, Daniel A.
? REGISTRATION NUMBER: 30'480
? REFERENCE/DOCKET NUMBER: 6056-173
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (215) 568-8383
? TELEFAX: (215) 568-5549
? TELEX: No. 5380646e
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 73 amino acids
? TYPE: AMINO ACID
? TOPOLOGY: linear
US-07-965-674-14

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Query Match	Score	DB 1;	Length
87.4%	334;	DB 1;	73;
84.4%	334;	DB 1;	73;

Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY      2 APANPCDDAATCKLTTSQCABDLCCDDCKFMKEGTVCRRARGDLDLDCNGISAGCPRN 61
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Db     10 SPANPCDAATCKLPGAQCGEGSLCCDDCSFMKGTICRRARGDLDLDCNGISAGCPRN 69
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QY	62	PFHA	65
Db	70	PLHA	73

RESULT 7  
US-08-993-165-15

; Patent No. 6123923  
; GENERAL INFORMATION:  
; INFORMATION:

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; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224

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; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 15
; LENGTH: 73
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
; OS-08-993-165-15

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Query Match	87.4%;	Score 334;	DB 3;	Length 73;
Best Local Similarity	84.4%;	Pred. No. 3.2e-26;		
Matches 54;	Conservative 5;	Mismatches 5;	Indels 0;	Gaps 0

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QY	62	PFHA	65
Db	70	PLHA	73

RESULT 8  
US-09-243-640-13  
; Sequence 13, Application US/09243640

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; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: shen, Dekang

```

: APPLICANT: Wu, Guang  
 : TITLE OF INVENTION: No. 6521211 Method Of Imaging And Treatment With Targeted  
 : TITLE OF INVENTION: Compositions  
 : TITLE OF INVENTION: Compositions

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; FILE REFERENCE: DUP-0463
; CURRENT APPLICATION NUMBER: US/09/243,640

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? CURRENT FILING DATE: 1999-02-03
? PRIOR APPLICATION NUMBER: 08/660,032
? PRIOR FILING DATE: 1996-06-06
? PRIOR APPLICATION NUMBER: 08/640,464
? PRIOR FILING DATE: 1996-05-01
? PRIOR APPLICATION NUMBER: 08/497,684
? PRIOR FILING DATE: 1995-06-07
? PRIOR APPLICATION NUMBER: 09/218,660
? PRIOR FILING DATE: 1998-12-22
? PRIOR APPLICATION NUMBER: 60/073,913
? PRIOR FILING DATE: 1998-02-06
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 13
? LENGTH: 73
? TYPE: PR1
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: No. 6521211el Sequence
? IS-09-243-640-13

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Query Match	87.4%	Score 334	DB 4	Length 73
Best Local Similarity	84.4%	Pred. No. 3.2e-26		
Matches 54	Conservative 5	Mismatches 5	Indels 0	Gaps 0

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QY	62	PFHA	65
Db	70	PLHA	73

RESULT 9  
US-08-929-847-15  
; Sequence 15, Application US/08929847

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; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Therm
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; CURRENT APPLICATION NUMBER: US/08/929, 847  
 ; CURRENT FILING DATE: 1997-09-15  
 ; NUMBER OF SEQ ID NOS: 39

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; COL NAME: FACILITY POSITION 3
; SEQ ID NO 15
; LENGTH: 73
; TYPE: PRT

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; ORGANISM: Streptococcus pyogenes
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; FEATURE:
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; OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-15

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Query Match	87.4%	Score 334;	DB 4;	Length 73;
Best Local Similarity	84.4%;	Pred. No. 3.2e-26;		
Matches	54:	Conservative	5:	Mismatches
			5:	Indels
			0:	Gaps
			0:	

QY 2 APANPCDDATCKLTTGSGCADGLCCDQC FMEKGTVRRARGDDLDPYCNGISAGCPRN 61  
:  
Db 10 SPANPCDDATCKLTGAGCGELCCDQCSFMKGGTTCRRARGDDLDPYCNGISAGCPRN 69

QY	62	PFHA	65
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RESULT 10  
US-09-460-295B-9  
: Sequence 9, Application US/09460295B

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; Patent NO. 6710030
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; GENERAL INFORMATION:
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; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA

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/ TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
/ TITLE OF INVENTION: OTHER CONDITIONS
/ FILE REFERENCE: 1279-338C3/09801388
/ CURRENT APPLICATION NUMBER: US/09/460,295B
/ CURRENT FILING DATE: 1999-12-10
/ PRIOR APPLICATION NUMBER: US 09/163,047
/ PRIOR FILING DATE: 1998-09-29
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 9
/ LENGTH: 73
/ TYPE: PRT
/ ORGANISM: Trimeresurus albolabris
/ US-09-460-295B-9

Query Match      87.4%; Score 334; DB 4; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 APANPCDAATCKLTGSGCADGLCCDQCKFMKEGTVCRARAGDDLDDYCNGISAGCPRN 61
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DB      10 SPANPCDAATCKLPGAGCGEGLCCDQCSFMKKGITCRARAGDDLDDYCNGISAGCPRN 69
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QY      62 PFHA 65
      :|||
DB      70 PLHA 73

RESULT 11
US-09-813-484-15
/ Sequence 15, Application US/09813484
/ Patent No. 6716412
/ GENERAL INFORMATION:
/ APPLICANT: Unger, Evan C.
/ TITLE OF INVENTION: No. 6716412el Methods Of Ultrasound Treatment Using Gas Or Gaseou
/ FILE REFERENCE: UNKRL600
/ CURRENT APPLICATION NUMBER: US/09/813,484
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 08/929,847
/ PRIOR FILING DATE: 1997-09-15
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 15
/ LENGTH: 73
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Completely sythetic sequence
/ US-09-813-484-15

Query Match      87.4%; Score 334; DB 4; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 APANPCDAATCKLTGSGCADGLCCDQCKFMKEGTVCRARAGDDLDDYCNGISAGCPRN 61
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DB      10 SPANPCDAATCKLPGAGCGEGLCCDQCSFMKKGITCRARAGDDLDDYCNGISAGCPRN 69
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QY      62 PFHA 65
      :|||
DB      70 PLHA 73

RESULT 12
PCT-US93-09523-14
/ Sequence 14, Application PC/TUS9309523
/ GENERAL INFORMATION:
/ APPLICANT: Temple University - Of The Commonwealth
/ APPLICANT: System of Higher Education
/ APPLICANT: Knight, Linda C. and
/ APPLICANT: Maurer, Alan H.
/ TITLE OF INVENTION: Thrombus Detection Using
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/ TITLE OF INVENTION: Radiolabelled Disintegrins
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Temple University - Of The
/ STREET: 406 University Services Building
/ CITY: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: U.S.A.
/ ZIP: 19122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: Wordperfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/09523
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 965,674
/ FILING DATE: 19 October 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Monaco, Daniel A.
/ REGISTRATION NUMBER: 30,480
/ REFERENCE/DOCKET NUMBER: 6056-173 PC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-8383
/ TELEFAX: (215) 568-5549
/ TELEX: None
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 73 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ PCT-US93-09523-14

Query Match      87.4%; Score 334; DB 5; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 APANPCDAATCKLTGSGCADGLCCDQCKFMKEGTVCRARAGDDLDDYCNGISAGCPRN 61
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DB      10 SPANPCDAATCKLPGAGCGEGLCCDQCSFMKKGITCRARAGDDLDDYCNGISAGCPRN 69
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QY      62 PFHA 65
      :|||
DB      70 PLHA 73

RESULT 13
US-09-776-268A-1
/ Sequence 1, Application US/09776268A
/ Patent No. 6537551
/ GENERAL INFORMATION:
/ APPLICANT: KIM, DOO-SIK
/ APPLICANT: CHUNG, Kwang Hoe
/ APPLICANT: KANG, In-Cheol
/ TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT
/ FILE REFERENCE: 0136/1P733-US1
/ CURRENT APPLICATION NUMBER: US/09/776,268A
/ CURRENT FILING DATE: 2002-02-02
/ PRIOR APPLICATION NUMBER: US 09/335,088
/ PRIOR FILING DATE: 1999-06-17
/ PRIOR APPLICATION NUMBER: KR 99-20579
/ PRIOR FILING DATE: 1999-06-04
/ PRIOR APPLICATION NUMBER: KR 98-23778
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 1
/ LENGTH: 73
/ TYPE: PRT
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ORGANISM: Agkistrodon halys brevicaudus  
US-09-776-268A-1

Query Match 86.9%; Score 329; DB 4; Length 73;  
Best Local Similarity 84.4%; Pred. No. 5.1e-26;  
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY 62 PFHA 65  
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DB 70 PLHA 73

RESULT 14  
US-09-540-448-15  
; Sequence 15, Application US/09540448  
; Patent No. 6403056  
; GENERAL INFORMATION:  
; APPLICANT: Unger, Evan C.  
; TITLE OF INVENTION: Charged Lipids and Uses For The Same  
; FILE REFERENCE: UNGR1592  
; CURRENT APPLICATION NUMBER: US/09/540,448  
; CURRENT FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 08/925,353  
; PRIOR FILING DATE: 1997-09-08  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056e1 Sequence  
US-09-540-448-15

Query Match 86.1%; Score 329; DB 4; Length 73;  
Best Local Similarity 82.8%; Pred. No. 1e-25;  
Matches 53; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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DB 10 SPANCCDAATCKLPGAGCGEGLCCDQCFMKEGTVCRARGDDLDDYCNGISAGCPNN 69

QY 62 PFHA 65  
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DB 70 PLHA 73

RESULT 15  
US-10-046-801-15  
; Sequence 15, Application US/10046801  
; Patent No. 6808720  
; GENERAL INFORMATION:  
; APPLICANT: Unger, Evan C.  
; TITLE OF INVENTION: Charged Lipids and Uses For The Same  
; FILE REFERENCE: UNGR1592  
; CURRENT APPLICATION NUMBER: US/10/046,801  
; CURRENT FILING DATE: 2002-05-13  
; PRIOR APPLICATION NUMBER: US/09/540,448  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 08/925,353  
; PRIOR FILING DATE: 1997-09-08  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 73  
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; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6808720e1 Sequence

US-10-046-801-15

Query Match 86.1%; Score 329; DB 4; Length 73;  
Best Local Similarity 82.8%; Pred. No. 1e-25;  
Matches 53; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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DB 10 SPANCCDAATCKLPGAGCGEGLCCDQCFMKEGTVCRARGDDLDDYCNGISAGCPNN 69

QY 62 PFHA 65  
||||  
DB 70 PLHA 73

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Job time : 43 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:14:38 ; Search time 169 Seconds  
(without alignments)  
160.927 Million cell updates/sec

Title: US-10-712-584-2\_COPY\_419\_483

Perfect score: 382

Sequence: 1 DAPANPCDDAATCKLTGSGQ.....DUDYCNIGSACPRNFHA 65

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Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	382	100.0	483	US-10-439-532-2	Sequence 2, Appli
2	382	100.0	483	US-10-712-584-2	Sequence 2, Appli
3	346	90.6	73	US-10-089-473A-10	Sequence 10, Appli
4	346	90.3	73	US-10-089-473A-1	Sequence 1, Appli
5	334	87.4	73	US-09-813-484-15	Sequence 15, Appli
6	334	87.4	73	US-10-439-532-9	Sequence 9, Appli
7	334	87.4	73	US-10-712-584-9	Sequence 9, Appli
8	329	86.9	73	US-09-776-268A-1	Sequence 1, Appli
9	329	86.1	73	US-10-046-801-15	Sequence 15, Appli
10	322	84.3	552	US-10-439-532-8	Sequence 8, Appli
11	322	84.3	552	US-10-712-584-8	Sequence 8, Appli

12	321.5	84.2	71	10	US-09-832-501-37	Sequence 37, Appli
13	321.5	84.2	71	14	US-10-439-532-7	Sequence 7, Appli
14	321.5	84.2	71	16	US-10-712-584-7	Sequence 7, Appli
15	286	74.9	478	14	US-10-078-866-2	Sequence 2, Appli
16	266	69.6	73	14	US-10-439-532-10	Sequence 10, Appli
17	266	69.6	73	16	US-10-712-584-10	Sequence 10, Appli
18	265	69.4	111	9	US-09-921-823-23	Sequence 23, Appli
19	265	69.4	195	9	US-09-921-823-8	Sequence 8, Appli
20	261	68.3	71	15	US-10-383-588A-6	Sequence 6, Appli
21	261	68.3	463	15	US-10-383-588A-2	Sequence 2, Appli
22	261	68.3	481	15	US-10-383-588A-8	Sequence 8, Appli
23	258	67.5	69	9	US-09-813-484-14	Sequence 16, Appli
24	244	63.9	70	9	US-09-813-484-17	Sequence 17, Appli
25	244	63.9	70	14	US-10-046-801-17	Sequence 14, Appli
26	243	63.6	69	14	US-10-046-801-14	Sequence 9, Appli
27	241.5	63.2	70	10	US-09-961-656-9	Sequence 16, Appli
28	238.5	62.4	68	14	US-10-046-801-16	Sequence 16, Appli
29	238.5	62.4	68	14	US-10-439-532-11	Sequence 11, Appli
30	228	59.7	68	16	US-10-712-584-11	Sequence 11, Appli
31	228	59.7	68	16	US-10-439-532-14	Sequence 14, Appli
32	228	59.7	478	16	US-10-712-584-14	Sequence 14, Appli
33	228	59.7	478	16	US-09-921-823-2	Sequence 2, Appli
34	223	58.4	400	9	US-09-921-823-17	Sequence 17, Appli
35	219	57.3	611	9	US-10-482-925A-1	Sequence 1, Appli
36	214	56.0	616	18	US-09-877-843-88	Sequence 88, Appli
37	207.5	54.3	76	10	US-09-877-843-88	Sequence 12, Appli
38	199	52.1	606	14	US-10-439-532-12	Sequence 12, Appli
39	199	52.1	606	16	US-10-712-584-12	Sequence 109, Appli
40	197	51.6	282	9	US-09-840-277-109	Sequence 13, Appli
41	195.5	51.2	571	14	US-10-439-532-13	Sequence 13, Appli
42	195.5	51.2	571	16	US-10-712-584-13	Sequence 8, Appli
43	191	50.0	49	9	US-09-840-277-8	Sequence 92, Appli
44	191	50.0	49	15	US-10-360-101-92	Sequence 1132, Appli
45	191	50.0	49	20	US-11-066-697-1132	

#### ALIGNMENTS

RESULT 1  
US-10-439-532-2  
; Sequence 2, Application US/10439532  
; Publication No. US20030186884A1  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA  
; TITLE OF INVENTION: CONTOURSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST  
; FILE REFERENCE: 1279-338N2/09801388  
; CURRENT APPLICATION NUMBER: US/10/439,532  
; CURRENT FILING DATE: 2003-05-16  
; PRIOR APPLICATION NUMBER: US09/591,552  
; PRIOR FILING DATE: 2000-06-08  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 483  
; TYPE: PRT  
; ORGANISM: Agkistrodon contortrix  
US-10-439-532-2

Query Match 100.0%; Score 382; DB 14; Length 483;

Best Local Similarity 100.0%; Pred. No. 6.1e-32;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	NPFA 65	
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RESULT 2
US-10-712-584-2
; Sequence 2, Application US/10712584
; Publication No. US20040132659A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; APPLICANT: Markland, Francis S.
; APPLICANT: Riteer, Matthew
; TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; FILE REFERENCE: 1279-338N3/09801388
; CURRENT APPLICATION NUMBER: US/10/712,584
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US09/591,552
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 08/141,321
; PRIOR FILING DATE: 1993-10-22
; PRIOR APPLICATION NUMBER: US 08/540,423
; PRIOR FILING DATE: 1995-10-10
; PRIOR APPLICATION NUMBER: US 08/632,691
; PRIOR FILING DATE: 1996-04-15
; PRIOR APPLICATION NUMBER: US 08/745,603
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: US 09/163,047
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: US09/460,295
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PR
; ORGANISM: Agkistrodon contortrix
US-10-712-584-2

Query Match          100.0%; Score 382; DB 16; Length 483;
Best Local Similarity 100.0%; Pred. No. 6,1e-32;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAPNPCCAAATCKLTTSQCADGLCCDCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN 60
DB 419 DAPNPCCAAATCKLTTSQCADGLCCDCKFMKEGTVCRRARGDDLDDYCNGISAGCPR 478

QY 61 NPFA 65
DB 479 NPFA 483

RESULT 3
US-10-089-473A-10
; Sequence 10, Application US/10089473A
; Publication No. US20050032189A1
; GENERAL INFORMATION:
; APPLICANT: CHUNG, Kwang-Hoe
; APPLICANT: KIM, Doo-Sik
; APPLICANT: KOH, You-Seok
; APPLICANT: SOHN, Young-Dong
; APPLICANT: YOU, Weon-Kyoo
; APPLICANT: JANG, Yang-Seo
; APPLICANT: HUH, Chin-Kyu
; TITLE OF INVENTION: NOVEL PROTEIN DERIVED FROM AGKISTRODON SAXATILIS EMELIANOV AND PR
; FILE REFERENCE: 0136/0K432USO
; CURRENT APPLICATION NUMBER: US/10/089,473A
; CURRENT FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 73
; TYPE: PR
; ORGANISM: Agkistrodon halys brevicaudus
US-10-089-473A-10
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Best Local Similarity 87.5%; Pred. No. 6,9e-29;
Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 APANPCDAAATCKLTTSQCADGLCCDCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN 61
DB 10 SPANPCDAAATCKLRGAQACAGLCCDCKFMKEGTICRRARGDDLDDYCNGISAGCPRN 69

QY 62 PFHA 65
DB 70 PFHA 73

RESULT 4
US-10-089-473A-1
; Sequence 1, Application US/10089473A
; Publication No. US20050032189A1
; GENERAL INFORMATION:
; APPLICANT: CHUNG, Kwang-Hoe
; APPLICANT: KIM, Doo-Sik
; APPLICANT: KOH, You-Seok
; APPLICANT: SOHN, Young-Dong
; APPLICANT: YOU, Weon-Kyoo
; APPLICANT: JANG, Yang-Seo
; APPLICANT: HUH, Chin-Kyu
; TITLE OF INVENTION: NOVEL PROTEIN DERIVED FROM AGKISTRODON SAXATILIS EMELIANOV AND PR
; FILE REFERENCE: 0136/0K432USO
; CURRENT APPLICATION NUMBER: US/10/089,473A
; CURRENT FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 73
; TYPE: PR
; ORGANISM: Agkistrodon saxatilis emelianov
US-10-089-473A-1

Query Match          90.3%; Score 345; DB 17; Length 73;
Best Local Similarity 87.5%; Pred. No. 8,8e-29;
Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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DB 10 APANPCDAAATCKLRGAQACAGLCCDCKFMKEGTICRRARGDDLDDYCNGISAGCPRN 69

QY 62 PFHA 65
DB 70 PFHA 73

RESULT 5
US-09-813-484-15
; Sequence 15, Application US/09813484
; Publication No. US20010031243A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: 6716412e1 Methods Of Ultrasound Treatment Using Gas Or Gaseou
; FILE REFERENCE: UNGR1600
; CURRENT APPLICATION NUMBER: US/09/813,484
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/929,847
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 73
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-09-813-484-15
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Query Match      87.4%; Score 334; DB 9; Length 73;
Best Local Similarity 84.4%; Pred. No. 1.3e-27;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 APANPCCDATKLTGSGCAGDLCCDQCKFMKEGTVCRARAGDDLDYCNGISAGCCPN 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      10 SPANPCCDATKLTLPAGACGEGGCCDQCSFMKKGTICRRARAGDDLDYCNGISAGCCPN 69

DB      62 PFHA 65
      |||
      70 PLHA 73

RESULT 6
US-10-439-532-9
; Sequence 9, Application US/10439532
; Publication No. US20030186884A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; TITLE OF INVENTION: CONTOPTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; TITLE OF INVENTION: OTHER CONDITIONS
; FILE REFERENCE: 1279-338N2/09801388
; CURRENT APPLICATION NUMBER: US/10/439,532
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US09/591,552
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Trimeresurus albolabris
US-10-439-532-9

Query Match      87.4%; Score 334; DB 14; Length 73;
Best Local Similarity 84.4%; Pred. No. 1.3e-27;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 APANPCCDATKLTGSGCAGDLCCDQCKFMKEGTVCRARAGDDLDYCNGISAGCCPN 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      10 SPANPCCDATKLTLPAGACGEGGCCDQCSFMKKGTICRRARAGDDLDYCNGISAGCCPN 69

DB      62 PFHA 65
      |||
      70 PLHA 73

RESULT 7
US-10-712-584-9
; Sequence 9, Application US/10712584
; Publication No. US20040132659A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; APPLICANT: Markland, Francis S.
; APPLICANT: Ralcer, Matthew
; TITLE OF INVENTION: CONTOPTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; TITLE OF INVENTION: OTHER CONDITIONS
; FILE REFERENCE: 1279-338N3/09801388
; CURRENT APPLICATION NUMBER: US/10/712,584
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US09/591,552
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 08/141,321
; PRIOR FILING DATE: 1993-10-22
; PRIOR APPLICATION NUMBER: US 08/540,423
; PRIOR FILING DATE: 1995-10-10
; PRIOR APPLICATION NUMBER: US 08/632,691
; PRIOR FILING DATE: 1996-04-15
; PRIOR APPLICATION NUMBER: US 08/745,603
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: US 09/163,047
; PRIOR FILING DATE: 1998-09-29
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; PRIOR APPLICATION NUMBER: US09/460,295
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Trimeresurus albolabris
US-10-712-584-9

Query Match      87.4%; Score 334; DB 16; Length 73;
Best Local Similarity 84.4%; Pred. No. 1.3e-27;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 APANPCCDATKLTGSGCAGDLCCDQCKFMKEGTVCRARAGDDLDYCNGISAGCCPN 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      10 SPANPCCDATKLTLPAGACGEGGCCDQCSFMKKGTICRRARAGDDLDYCNGISAGCCPN 69

DB      62 PFHA 65
      |||
      70 PLHA 73

RESULT 8
US-09-776-268A-1
; Sequence 1, Application US/09776268A
; Publication No. US20010023242A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Doo-Sik
; APPLICANT: CHUNG, Kwang Hoe
; APPLICANT: KANG, In-Cheol
; TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT
; FILE REFERENCE: 0136/1F733-US1
; CURRENT APPLICATION NUMBER: US/09/776,268A
; PRIOR FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: US 09/335,088
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: KR 99-20579
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: KR 98-23778
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Agkistrodon halys breviceaudus
US-09-776-268A-1

Query Match      86.9%; Score 332; DB 9; Length 73;
Best Local Similarity 84.4%; Pred. No. 2e-27;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 APANPCCDATKLTGSGCAGDLCCDQCKFMKEGTVCRARAGDDLDYCNGISAGCCPN 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      10 SPANPCCDATKLTLPAGACGEGGCCDQCKFMKEGTVCRARAGDDLDYCNGISAGCCPN 69

DB      62 PFHA 65
      |||
      70 PLHA 73

RESULT 9
US-10-046-801-15
; Sequence 15, Application US/10046801
; Publication No. US20030054027A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged lipids and Uses for The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/10/046,801
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448
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/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 08/925,353
/ PRIOR FILING DATE: 1997-09-08
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 15
/ LENGTH: 73
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027A1 Sequenc
US-10-046-801-15

Query Match
Best Local Similarity 86.1%; Score 329; DB 14; Length 73;
Matches 53; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDDATCKLTGSGCAGDGLCCDCKFMKEGTVCRARGDDLDDYCNIGISAGCPRN 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 10 SPANPCDDATCKLIPGACGEGGLCCDCKSFMEKGTICRRARGDDLDDYCNIGISAGCPRN 69

QY 62 PFHA 65
:|||||
DB 70 PFHA 73

RESULT 10
US-10-439-532-8
/ Sequence 8, Application US/10439532
/ Publication No. US20030186884A1
/ GENERAL INFORMATION:
/ APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
/ TITLE OF INVENTION: CONFOROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
/ FILE REFERENCE: 1279-338N2/09801388
/ CURRENT APPLICATION NUMBER: US/10/439,532
/ PRIOR FILING DATE: 2003-05-16
/ PRIOR APPLICATION NUMBER: US09/591,552
/ PRIOR FILING DATE: 2000-06-08
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8
/ LENGTH: 552
/ TYPE: PRF
/ ORGANISM: Trimeresurus gramineus
US-10-439-532-8

Query Match
Best Local Similarity 84.3%; Score 322; DB 14; Length 552;
Matches 53; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 APANPCDDATCKLTGSGCAGDGLCCDCKFMKEGTVCRARGDDLDDYCNIGISAGCPRN 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 489 SPANPCDDATCKLIPGACGEGGLCCDCKSFMEKGTICRRARGDDLDDYCNIGISAGCPRN 548

QY 62 PFHA 65
:|||||
DB 549 PFHA 552

RESULT 11
US-10-712-584-8
/ Sequence 8, Application US/10712584
/ Publication No. US20040132659A1
/ GENERAL INFORMATION:
/ APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
/ APPLICANT: Markland, Francis S.
/ APPLICANT: Riteer, Matthew
/ TITLE OF INVENTION: CONFOROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
/ FILE REFERENCE: 1279-338N3/09801388
/ CURRENT APPLICATION NUMBER: US/10/712,584
/ CURRENT FILING DATE: 2003-11-12
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```
/ PRIOR APPLICATION NUMBER: US09/591,552
/ PRIOR FILING DATE: 2000-06-08
/ PRIOR APPLICATION NUMBER: US 08/141,321
/ PRIOR FILING DATE: 1993-10-22
/ PRIOR APPLICATION NUMBER: US 08/540,423
/ PRIOR FILING DATE: 1995-10-10
/ PRIOR APPLICATION NUMBER: US 08/632,691
/ PRIOR FILING DATE: 1996-04-15
/ PRIOR APPLICATION NUMBER: US 08/745,603
/ PRIOR FILING DATE: 1996-11-08
/ PRIOR APPLICATION NUMBER: US 09/163,047
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: US09/460,295
/ PRIOR FILING DATE: 1999-12-10
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8
/ LENGTH: 552
/ TYPE: PRF
/ ORGANISM: Trimeresurus gramineus
US-10-712-584-8

Query Match
Best Local Similarity 84.3%; Score 322; DB 16; Length 552;
Matches 53; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 APANPCDDATCKLTGSGCAGDGLCCDCKFMKEGTVCRARGDDLDDYCNIGISAGCPRN 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 489 SPANPCDDATCKLIPGACGEGGLCCDCKSFMEKGTICRRARGDDLDDYCNIGISAGCPRN 548

QY 62 PFHA 65
:|||||
DB 549 PFHA 552

RESULT 12
US-09-832-501-37
/ Sequence 37, Application US/09832501
/ Publication No. US20030199043A1
/ GENERAL INFORMATION:
/ APPLICANT: Ballance, David J.
/ APPLICANT: Sleep, Darrell
/ APPLICANT: Turner, Andrew J.
/ APPLICANT: Sadegh, Homa
/ APPLICANT: Prior, Christopher P.
/ TITLE OF INVENTION: Albumin Fusion Proteins
/ FILE REFERENCE: PF542
/ CURRENT APPLICATION NUMBER: US/09/832,501
/ CURRENT FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/229,358
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: 60/256,931
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/199,384
/ PRIOR FILING DATE: 2000-04-25
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 37
/ LENGTH: 71
/ TYPE: PRF
/ ORGANISM: Agkistrodon piscivorus
US-09-832-501-37

Query Match
Best Local Similarity 84.2%; Score 321.5; DB 10; Length 71;
Matches 54; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 2 APANPCDDATCKLTGSGCAGDGLCCDCKFMKEGTVCRARGDDLDDYCNIGISAGCPRN 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 10 SPANPCDDATCKLIPGACGEGGLCCDCKFMKEGTVCRARGDDLDDYCNIGISAGCPRN 68

QY 62 PFH 64
:|||||
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Db 69 PFH 71

## RESULT 13

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US-10-439-532-7
; Sequence 7, Application US/10439532
; Publication No. US20030186884A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; TITLE OF INVENTION: CONTOURSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; FILE REFERENCE: 1279-338N2/09801388
; CURRENT FILING DATE: 2003-05-16
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Agkistrodon piscivorus
US-10-439-532-7
```

```
Query Match 84.2%; Score 321.5; DB 14; Length 71;
Best Local Similarity 85.7%; Pred. No. 2,5e-26;
Matches 54; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
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QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRARDDDDLDYCNISAGCPRN 61

Db 10 SPENPCDDAATCKLRGQAQCAEGLCCDCKFMKEGTVCRARDDVDVNDYCNISAGCPRN 68

QY 62 PFH 64  
Db 69 PFH 71

## RESULT 14

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US-10-712-584-7
; Sequence 7, Application US/10712584
; Publication No. US20040132659A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; APPLICANT: Markland, Francis S.
; APPLICANT: Ritter, Matthew
; TITLE OF INVENTION: CONTOURSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; FILE REFERENCE: 1279-338N3/09801388
; CURRENT FILING DATE: 2003-11-12
; PRIOR FILING DATE: 2000-06-08
; PRIOR FILING DATE: 2000-06-08
; PRIOR FILING DATE: 1993-10-22
; PRIOR FILING DATE: 1995-10-10
; PRIOR FILING DATE: 1995-10-10
; PRIOR FILING DATE: 1996-04-15
; PRIOR FILING DATE: 1996-11-08
; PRIOR FILING DATE: 1998-09-29
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Agkistrodon piscivorus
US-10-712-584-7
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Query Match 84.2%; Score 321.5; DB 16; Length 71;

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Best Local Similarity 85.7%; Pred. No. 2,5e-26;
Matches 54; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
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QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRARDDDDLDYCNISAGCPRN 61

Db 10 SPENPCDDAATCKLRGQAQCAEGLCCDCKFMKEGTVCRARDDVDVNDYCNISAGCPRN 68

QY 62 PFH 64  
Db 69 PFH 71

## RESULT 15

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US-10-078-866-2
; Sequence 2, Application US/10078866
; Publication No. US20030096393A1
; GENERAL INFORMATION:
; APPLICANT: FOX, BRIAN A
; APPLICANT: SHEPPARD, PAUL O.
; TITLE OF INVENTION: Disintegrin Homolog, zanki6
; FILE REFERENCE: 01-05
; CURRENT FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-10-078-866-2
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Query Match 74.9%; Score 286; DB 14; Length 478;
Best Local Similarity 73.4%; Pred. No. 7,3e-22;
Matches 47; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
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QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRARDDDDLDYCNISAGCPRN 61

Db 415 SPANPCDDAATCKLRGQAQCAEGLCCDCKFMKEGTVCRARDDVDVNDYCNISAGCPRN 474

QY 62 PFH 65  
Db 475 PFH 478

Search completed: November 3, 2005, 08:23:19  
Job time : 171 secs

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## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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